

STIC Database Tracking Number: 95244

TO: Manjunath N Rao

Location: cm1/10a/11/10d01

Art Unit: 1652

Monday, June 09, 2003

10

Case Serial Number: 1005499

From: Edward Hart

Location: Biotech-Chem Library

CM1-6B02

Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Rao,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



1)

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Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into to two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, .rnpm and .rnpn
Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, .rapm and .rapn

The Pending database search results should not be left in the case because they contain data that is confidential.

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STIC-Biotech/ChemLib

95244

Fr m: Sent:

Rao, Manjunath N.

Friday, May 23, 2003 2:54 PM

T:

STIC-Biotech/ChemLib

Subject:

Sequence search request for 10/005,499

Fr.m: Manjunath N. Rao

Art Unit 1652, Room 10A11 Mail Box in Room 10D 01

Phone: 306-5681

Date: 5-23-03

Please search the following as soon as possible for application with serial number 10/005499

- 1. SEQ ID NO: 377 against all <u>commercial nucleic acid databases</u> including <u>issued patents database</u> and <u>pending application database</u> and provide a <u>print of all results</u>.
- 2. SEQ ID NO:378 against all <u>commercial protein databases</u> including <u>issued patents database</u> and <u>pending</u> <u>application database</u> and provide a <u>print of all results</u>.

If y u have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao, Ph.D. Bi technology Patent Examiner Art Unit 1652, Room 10A11 Mail Box in 10D01 Crystal Mall 1, USPTO. Edward Harl Technicai Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

Searcher:
Phone:
Location:
Date Picked Up: 6/2/103
Date Completed: 1/9/103
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:/
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)	
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WWW/Internet:	
Other (specify):	
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STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Same Barabah	
> I an	n an examiner in Workgroup: Example: 1610
> Rele	evant prior art found , search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	☐ Foreign Patent(s)
	☐ Non-Patent Literature
	(journal articles, conference proceedings, new product announcements etc.)
> Rele	evant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Comme	ents:

Drop/off or send completed forms to STIC/Biotech₌Chem:Library,CM1≔Circ: Desk



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AC026125

AC026125
Homo sapiens chromosome 12 clone RP11-234P5, WORKING DRAFT
AC026125. 14 unordered pieces.
AC026125. 22 GI:21430995
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Human.
Humo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Putheria; Primates; Catarrhini; Hominidae; Homo.
I (Dases 1 to 175186)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,

RESULT 1 AC026125 LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS

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NOTE: Estimated insert size may differ from sequence length
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Barbarla, J., Benton, J., Blmage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowles, S., Britava, M., Brown, E., Brown, M., Bryant, N.P., Bulkey, C., Burch, P., Burket, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, R., Chan, R., Chodhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, R., David, R., David, M., David, M.D., Dathorne, S.R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H., Douthwatter, K.J., Drager, D., Edwards, C.C., Elhaj, C., Esoctto, M., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Esotto, M., Falls, T., Ferraguto, D., Edwards, C., Elhaj, C., Esotto, P., Frantz, P., Gorfell, T., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Honson, R., Gollvet, S., Joudah, S., Kratcovic, J., Kratcovic, J., Kratcovic, J., Kratcovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Loulseged, H., Lozaco, B., Martin, Y., Martin, R., Martin, M., Mayue, P., Martin, R., Martin, M., Mayue, M., Okuedo, R., Martin, Y., Martin, R., Martin, M., Mayue, M., Okuedo, R., Martin, R., Martin, R., Martin, M., Mayue, M., Okuedo, R., Martin, R., Martin, M., Mayue, M., Martin, M., Mart
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Submitted (18-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 17, 2002 this sequence version replaced gi:20336719.
Center: Baylor College of Medicine
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Submitted (19-MAR-2000) Human Genome Sequencing Center, Department
Of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 175186)
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Web site: http://www.hgsc.bcm.tmc.edu/
Drafting Center Code: BCM
Contect: hgsc-help@bcm.tmc.edu
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Center clone name: RP11-234P5
------- Summary Statistics
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2 (bases 1 to 175186)
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TITLE

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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Manmalla Eutherla; Primates; Catarrhini; Hominidae; Homo.

Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-Osman, F. R., Allen, C.,

Alsbrocks, S.L., Amaratunge, H.C., Arej, R., Ayele, M., Bonnin, D.,

Boucki, J., Bowde, S., Brieve, R., Brown, B., Bryant, N.P.,

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Carron, T. E., Carter, M., Cavazos, S.R.; Chackor, J. Chavez, D.,

Chen, G., Chen, R., Chen, Z., Chowdhry, I. Christopoulos, C.,

Cleveland, C.D., Cox, C., Coyle, M.D., Dathone, S.R., David, R.,

Davilan, L., Days, C., Dayy-Carroll, L., Dederich, D. A.,

Delaney, K.R., Delgar, D., Edward, M., Stone, R., Durbin, K.J.,

Earnhart, C., Edgar, D., Edward, C., Coyle, M., Fealls, T., Earnhart, C., Edgar, D., Edward, C., Chulins, B.,

Earlhart, C., Edgar, D., Edward, C., Challo, T., Poster, P., Frantz, P.,

Gorrell, J. H., Guevar, W., Gunarathe, P., Hale, S., Hamilton, K.,

Harris, C., Harris, K., Hart, M., Haves, A., Hernandez, J.,

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Rives, M., Rojae, R., Pathus, E., Pan, P., Tamerisa, R., Tann, H.,

Scherer, S., Scott, G., Zhen, H., Shooshtari, N., Stone, H.,

Sutton, A., Syatek, A., Palbor, J., Stone, H.,

Sutton, A., Syatek, A., Warten, R., Washington, C., Wang, S., Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (29-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Agylor Plaza, Houston, TX 77030, USA (bases 1 to 194578)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Aug 22, 2002 this sequence version replaced g1:21954865.

Center: Baylor College of Medicine
Primates; Catarrhini; Hominidae; Homo.
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Contact: hgsc-help@bcm.tmc.edu
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Worley, K.C.
Direct Submission
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Web site: http://
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Unpublished
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Homo sapiens clone RP11-161H23, *** SEQUENCING IN PROGRESS ***, 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                148715 ACTGAACGGGAGGGTACTAGAGGACCACTGGCTCTGGACCGTCGGGAGCTGCCCTGACG
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               ACTGAACGGGAGGGTACTAGAGGACCACTGGCTCTGGACCGTCGGGAGCTGCCCTGACG
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HTG; HTGS_PHASE2; HTGS_ACTIVEFIN
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers

Location/Qualifiers
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Iswaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammaliai Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 20760)

RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alabratia, J., Bantan, J., Blange, M.C., Alabratia, J., Benton, J., Blange, M.C., Blankenburg, K., Bonnin, D., Burbert, C., Burrell, K.L., Byrd, N.D., Carron, T.F., Carter, M., Cavacos, S.R., Chaveco, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davy-Carroll, L., Dederich, D., Bordarde, C.D., Davis, C., Elaj, C., Elaj, C., Escotto, M. Earnharte, C., Edgar, D., Edgar, D., Edgar, D., Edgar, D., Edgar, D., Edgar, D., Edgar, P., Frantz, P., Earnhart, C., Edgar, D., Elagg, N., Ford, J., Foster, P., Frantz, P., Garrie, A., Gao, J., Garrie, A., Garner, T., Garza, N., Gill, R., Harris, C., Harris, R., Hart, M., Havlak, S., Hume, J., Jackson, L.E., Jacobson, B., Johnson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, K., Howard, S., Chume, J., Kovar, C., Lewis, L., Li, J., Li, Z., Lichtage, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozado, R.J., Lu, X., Lucier, R., Lucier, Luc
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AC010173.24 GI:22002320 AC010173.24 GI:22002320 HTG; HTGS_PHASE1; HTGS_BRAFT; HTGS_FULLTOP.
777
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                                 111126 GGTGCACAGCTCCCGCGGGCCAGCGCATACAGATGCTGGGTCGCTGCCGCATGGTGTG
                                                                                                                                             CGACCCGCATGGGCCCCGTGGTCCCCGACGGCGCGCCTGCTTCCGTGCCTCCCTT
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Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Merzker, M., Massey, E., Mawhiney, E., Mitchell, T., Mohabat, K., Morgan, M., Morris, S., Moser, M., Nather, B., Mokenkwo, S., Oguh, M., Okwuon, G., Oragunye, N., Ovledo, R., Pace, M., Paton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Prims, E., Put, L.L., Oulles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Schere, S., Scott, G., Shen, H., Stooshtari, N., Sison, I., Sodergren, E., Sonaike, T., Stanley, H., Stone, H., Stone, H., Sutton, A., Svatek, A., Tamerisa, R., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Walliams, G., Williamson, R., Warlington, C., Watlington, S., Walliams, G., Williamson, A., Waleczyk, R., Wooden, S., Worley, K., Weinstock, G. and Gibbs, R.
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NOTE: This is a "working draft' sequence It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Worley, K.C.
Direct Submitssion
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 29, 2002 this sequence version replaced gi:21954835.
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Chemistry: Dye-terminator Big Dye: 70% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 202882 bases at least Q40
Consensus quality: 203920 bases at least Q30
Consensus quality: 204475 bases at least Q30
Estimated insert size: 204019; sum-of-contigs estimation
Quality coverage: 9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-SEP-1999) Human Genome Sequencing Center, Departmer of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 207607)
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gap of unknown length
contig of 30205 bp in length
gap of unknown length
contig of 46200 bp in length
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Center code: BCM
Web Site: http://www.hgsc.bcm.tmc.edu/
Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
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------ Summary Statistics
Sequencing vector: M13;
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Center clone name: RP11-9
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152273: contig of 42038 bp in length
152373: gap of unknown length
207607: contig of 55234 bp in length.
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                                                                                                                                                                Score 1172.8; DB 2
Pred. No. 2.9e-157;
0; Mismatches 2;
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                                                                                                            clone="RP11-977B10"
49478 c 48758 g 54912
                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                           Location/Qualifiers
                                                                                                 /chromosome="12"
                                                                                                                                                                   58.2%;
99.5%;
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Best Local Similarity 99.5
Matches 1218; Conservative
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Worley, K.C.
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Alsbrooks, L., Andratunge, H.C., Are, J.R., Ayele, M., Banks, T., Blazbrooks, S.L., Andratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbrooks, S.L., Andratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbrooks, S.L., Andratunge, H.C., Are, J.R., Bonnin, D., Barbrooks, S.L., Brenton, J., Burkett, C., Burrell, R.L., Byrd, N.C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, G., Cov, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., David, R.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gorrell, J.H., Guevara, W., Ganner, T., Garza, N., Gill, R., Gao, J., Garcia, A., Havlak, P., Hawes, A., Hennandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jao, Y., Janks, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Lewis, L., Korvah, J., Karatovic, J., Kureshi, A., Ladi, Y., Luu, J., Liu, W., Loulseged, H., Louzado, R.J., Liu, X., Lucher, A., Lucker, R., Luu, J., Liu, W., Loulseged, H., Louzado, R.J., Liu, X., Lucher, A., Lucker, R., Lucker, R., Marshor, M., 
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                             CCCGCCAGGCGCCAAGGGAGGTGGGCCGGCGCGGGAAAGCAGGCCTGCGGGGGCCCCC
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Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, R., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Walliams, G., Walren, R., Washington, C., Watlington, S., Wulliamson, A., Wleczyk, R., Wooden, S., Worley, K., Weinstock, G. and Gibbs, R.

**March Submission**
**Direct Submi
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NOTE: This is a "working draft' sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:17972984.

Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center: Code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project name: GGWU
Center project name: GGWU
Center clone name: CH230-68F12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (30-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 177172)
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 114550 bases at least Q40
Consensus quality: 121322 bases at least Q20
Consensus quality: 121322 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                 172 AGAGCCCGGGACGTCCGGAGCGCGGGGAGCAGTCCCTCTCCATCAGGGAGTGGTCTATC 231
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Pred. No. 8.2e-85;
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Best Local Similarity 75.7%;
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Mammalla; Eutherla; Rodentla; Sclurognathi; Muridae; Murinae;
                             GGGGCCCCCTGGACCACCAGGTCCAAGAGGGCCCCCAGGAGACCCGGCAGGCCAGGCCC
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Atves, M. Kojas, A., Kojunokan, I., Kollewin, Kulz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tamerisa, A., Tamerisa, K., Tang, H., Tang, H., Tanger, J., Taylor, C., Taylor, T., Tabor, P., Villalon, D., Vinson, R., Wang, G., Wang, G., Warlen, Y., Warken, R., Washington, C., Watlidamson, A., Wleczyk, R., Wooden, S., Worley, K., Wallidamson, A., Wleczyk, R., Wooden, S., Worley, K., Wallidamson, A., Wleczyk, R., Wooden, S., Worley, K., Direct Submission

AL Upublished

S (Daylor Plaza, Houston)

AL Submitted (15-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

S (Daylor Plaza, Houston, TX 77030, USA)

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Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 12, 2002 this sequence version replaced gi:20514409.
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NOTE: This is a "working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is
Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G.,
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: htgsc-help@bcm.tmc.edu
Center project information
Center clone name: GRMO
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221470 bp DNA linear HTG 06-SEP-2000 Mus musculus clone RP23-121G4, WORKING DRAFT SEQUENCE, 40 unordered pieces.
AC027679.4 GI:9972295
HTG; HTGS_PHASEI; HTGS_DRAFT.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 221470)
McCombie,W.R., Baker,J.P., Bahret,A., Bal,H., Dedhia,N.N., de la
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                                                                                            Submitted (01-APR-2000) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, 19SA on Sep 6, 2000 this sequence version replaced g1:8493557.
Bastide, M., Huang, E.N., King, L., Kirchoff, K.A., Miller, B.,
Nascimento, L.U., O'Shaughnessy, A.L., Preston, R.R., Rodriguez, M.A.,
Shah, R.S., Shekher, M., Spiegel, L.A., Toth, K. and Vil, M.D.
Mouse Genomic Sequence
                                                                                                                                                          Center: Lita Annenberg Hazen Genome Center, Cold Spring Harbor
                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is
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Web site: http://www.cshl.org/genseq
Contact: mccomble@cshl.org
Contact: mccomble@cshl.org
Center: Project Information
Center project name: RP23-121G4
Center clone name: RP23-121G4
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    /organism="Mus musculus"
    /db_xref="taxon:10090"

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                                                          /note="CRF; contains a triple helical collagenous do
and a Clq signature domain; highly expressed in the
brainstem"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17q21"
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Berube,N.G., Swanson,H.X. and Pereira-Smith,O.M.
Direct Submission,H.X. huffington Center on Aging, Baylor College Submitted (28-SEP-1998) Huffington Center on Aging, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Berube, N.G., Swanson, H.X., Bertram, M.J., Kittle, J.D., Didenko, V., Baskin, D.S., Smith, J.R. and Pereira-Smith, O.M. Cloning and characterization of CRF, a novel Clq-related factor, expressed in areas of the brain involved in motor function
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                       CCCAGGGGAAGCCGGCCGCACCGGCAAGCCCGGGCCCTCCGGGGCCTCCCGGGGGACCCAG
                                               CGGGGCTGCCGGGGGGGGGGGGGGGGGCGCCATCAGCACTGCCACCTACACCACGGTGC
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       /translation="MVLLLVILIPVLVSSAGTSAHYEMLGTCRWVCDPYGGTKAPSTA
ATPDRGLMQSLPTFIQGPKGEAGRPGKAGPRGPPGPPGPPGPPGFPGEPGRQGLP
GPPGAPGLNAAGAISAATYSTVPKIAFYAGLKRQHEGYEVLKFDDVYTNLGNHYDPTT
GRPGAFGLYFFTHVLMRGGDGTSMWADLCKNNQVRASAIAQDADQNYDYASNSVV
LHLEPGDFVIKLDGGRAHGGNNKYSTFSGFIIYAD"
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                                                                                    2526;
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                                                                                                       257; Indels
                                                                                  Score 305.8; DB 10;
Pred. No. 3.5e-34;
0; Mismatches 257; I
/db_xref-"GI:10566471"
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/translation="MVLLLVILIPVLVSSAGTSAHYEMLGTCRWVCDPYGGTKAPSTA
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GRTCSIPGTYFFTYHVLMRGGDGTSWMADLCKNNQVRASAIAQDADQNYDYASNSVV
LHLEPGDEVIKLGGRAHGGNNNKYSTFSGFIIYAD"

276 c 284 g 1199 t
07-AUG-2002
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S., Martin, R.G., Muzny, D.M.,
                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 31 Row: f Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                      Mammalian
                        complete cds.
                                                                                                                                                                                                                                    Strausberg, R.

Direct Submission
Submitsted (01-MAR-2002) National Institutes of Health, Mammallan
Submitted (01-MGC), Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse."
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Tissue Procurement: Jeffrey E. Green, M.D.
TobNa Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.N.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
800
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bp mRNA linear
) IMAGE:4240136, mRNA,
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: angebcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly/
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart:
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="MGC:25969 INAGE:4240136"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV-SPORT6"
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BC024634 970 b
Mus musculus, clone MGC:25969
                                                                                                                                                               Chordata;
Rodentia;
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/codon_start=1
                                            BC024634
BC024634.1 GI:19353132
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1 (bases 1 to 970)
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Local S.
511;
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found

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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                               /translation="PHEGYEVLKFDDVVTNLGNNYDAASGKFTCNIPGTYFFTYHVLM
RGGDGTSMWADLCKNGQVRASAIAQDADQNYDYASNSVILHLDAGDEVFIKLDGGKAH
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 44 Row: f Column: 10.
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Pred. No. 3.7e-30;
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<1. .364
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83.0%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 847)
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                                                                                                                                                                                                                        ACAGGTCCGGGCCAGCGCCATTGCTCAGGACGGGGACCAGGAACTACGACTACGCCAGCAA
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                                                                                    GCCCCCCTTCCCGCCAGGCGCGCAAGGGAGAGGTGGGCCGGCGCGGGGAAAGCAGGCCTGCG
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mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                            TGGGCCCCGTGGCCCTGGTCCCGACGCCGCGCCTGC.
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Mus musculus, clone IMAGE:4503736,
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BC022724.1 GI:18490546
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Strausberg, R.
Direct Submission
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TITLE
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          Craniata; Vertebrata; Euteleostomi;
Catarrhin; Hominidae; Homo.
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                                                                                                                                                     Score 271.6; DB 6; Length
Pred. No. 2.6e-29;
0; Mismatches 209; Indels
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a 543 c 555 g 279 t
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Patent: WO 0248337-A 80 20-JUN-2002;
INCYTE GENOMICS INC (US)
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Sequence 1 from Patent WO0212475.
AX456049
Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                            Location/Qualifiers
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Similarity 65.8%;
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GFLLLYPD"
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Cid-related factor, homologous polypeptides and therapeutic uses thereof
Patent: WO 0212475-A 114-FEB-2002;
ELI LILLY AND COMPANY (US)
Location/Qualifiers
1. 981
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/ note="PRIMATE-1p231"
55. .732
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Sequence 1 from Patent WO0244373.
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Best Local Similarity 70.8
Matches 344; Conservative
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244 c 254 g 146 t
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                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0244373-A 1 06-JUN-2002;
ZymoGenetics. Inc. (US)
Location/Qualifiers
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   AX477323.1 GI:22216574
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Oligonucleotide fo Oligonucleotide fo Human CRF-like pro Oligonucleotide fo Oligonucleotide fo Oligonucleotide fo Oligonucleotide fo Oligonucleotide fo Mouse ischaemic co

> ABQ29323 ABQ29324 ABQ29325 ABI99588 ABK63764 AAS39926

ABK10666

Rat sequence different sequence of Human idestive sy Human foetal liver Human brain express Human brain express Human benome derive Monkey MANGO 245 D Human pelonal evil Human polynucleoti Human secreted pro Human secreted pro Human secreted pro Human adenosine Al

ABA59702 AAK07971 AAI395671 AAI39567 ABS08688 AAF28263 AAF28263 AAF28672 AAF4999 AAF45000

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Human adipocyte-sp CDNA clone encodin Human PRO344 nucle Human PRO344 prote Human PRO344 prote encoding nove Human PRO344 cDNA.

ALIGNMENTS

Human secreted pro Human secreted pro

AAF45001 AAF44970 AAF44998 AAX53491 AAF44994 AAF44996

a			Description	Gene encoding nove	Gene encoding nove	Murine HSP47 inter	Parallel detection	Human polynucleoti	Oligonucleotide fo	· Oligonucleotide fo	DNA encoding novel	Human ovarian canc
CHARMAC			QI .	ABK35597	ABK35598	AAH48068	AAH21084	ABA90355	ABQ45772	ABQ45773	AAS17577	ABL78241
			BB:	24	24	22	22	24	24	24	24	24
			re Match Length DB II	717	804	2526	639	768	584	584	864	466
	æ	Query	Match	35.6	30.8	15.2	15.1	15.0	14.2	14.2	13.5	13.3
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RESULT 1	
ABK35597	
ABK35597 standard; DNA; 717 BP.	
ABK35597;	
08-MAY-2002 (first entry)	
Gene encoding novel human secreted or membrane-associated protein #16.	rane-associated protein #16.
Human; secreted protein; membrane-associated protein; hypertension;	ed protein; hypertension;
inflammatory disorder; neurological disorder; haematopoietic disorder;	er; haematopoletic disorder;
skeletal developmental disorder; growth abnormality; autoimmune disorder;	normality; autoimmune disorder;
neurodegenerative disorder; nervous system disorder; bacterial infection;	disorder; bacterial infection;
peripheral myelinopathy; viral infection; cancer; obesity; diabetes;	cancer; obesity; diabetes;
hypotension; sexual development disorder; blood disorder; gene; ds.	blood disorder; gene; ds.
Homo sapiens.	
WO200204600-A2.	
17-JAN-2002.	
PF 12-JUL-2001; 2001WO-US21985.	
PR 12-JUL-2000; 2000US-218033P.	
21-AUG-2000; 2000US-226517P.	
(SMIK) SMITHKLINE BEECHAM CORP. (SMIK) SMITHKLINE BEECHAM PLC.	
PA (GLAX) GLAXO GROUP LTD.	
XX	

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or membrane-associated proteins and the genes encoding them. The sequences of the invention are useful for treating, preventing and ameliorating various diseases such as inflammatory disorders (e.g. asthma), neurological disorders (e.g. dementia), haematopoietic disorders, skeletal developmental disorders, growth abnormalities, neurodegenerative disorders (e.g. tuntington's disease), nervous system of sorders, autoimmune disorders (e.g. theumatorid arthritis), peripheral myelinopathies, viral and bacterial infections, alpha mannosidosis, diabetes, cancers, malignant tumours, hyper- and hypotension, obesity, bulimia, anorexia, manic depression, delirium, mental retardation, Tourette's syndrome, schizophrenia, growth, mental or sexual development disorders, and dysfunctions of the blood cascade constant including those leading to stroke, ABR35582-ABK35609 represent the genes encoding the novel human secreted or membrane-associated
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100.0%; Pred. No. 7.8e-122;
ive 0; Mismatches 0;
       Martensen SA,
                                                                                                                                                                                                                                   present invention relates to the isolation
                                                                                                                                                                                                  Claim 2; Page 110; 151pp; English.
     Lai Y,
Cogswell JP, Li
xiang Z, Xie Q;
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proteins of the invention
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nes 717; Conservative
                Xiang Z,
                                                        2002-188468/24
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                    Smith RF,
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The present invention relates to the isolation of novel human secreted or membrane-associated proteins and the genes encoding them. The sequences of the invention are useful for treating, preventing and membrorating various diseases such as inflammatory disorders (e.g. ameliorating various disorders (e.g. dementia), haematopoletic asthma), neurological disorders (e.g. dementia), haematopoletic disorders, skeletal developmental disorders, growth abnormalities, neurodegenerative disorders (e.g. theumatoid arthritis), peripheral myelinopathies, viral and bacterial infections, alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and phypotension, obesity, bulimia, anorexia, manic depression, delirium, mental retardation, Tourette's syndrome, schizophrenia, growth, mental or sexual development disorders, and dysfunctions of the blood cascade system including those leading to stroke. ABK15582-ABK13609 represent the genes encoding the novel human secreted or membrane-associated
                                                      ATTCTGCACCTGGACGTGGGCGACGACGTCTTCATCAAGCTGGACGGCGGGAAAGTGCAC 1342
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601 ATTCTGCACCTGGACGTGGGCGACGACGTCTTCATCAAGCTGGACGGCGGGAAAGTGCAC
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                                                                                                                                                         secreted protein; membrane-associated protein; hypertension;
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                               87;
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       other;
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                 Score 620; DB 24;
Pred. No. 3.7e-104;
0; Mismatches 0;
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      A; 293
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Best Local Similarity 89.2%;
Matches 717; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method for preparing a protein which interacts with the heat shock protein H8747. The method involves the two-hybrid screening method using the H8747 gene and a mammalian CDNA library. The present sequence is the coding sequence for a murine H8747 interacting protein which was used in the present method. The H8747 interacting proteins are useful for the diagnosis and treatment of diseases caused by an increase or decrease in activity of H8747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            940 AGCTCGGCCGGCACGTCGGCTCACTACGAGATGCTGGGCACCTGCCGCATGGTCTGCGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                  Using the two-hybrid screening method to prepare proteins which interact with the heat shock protein {\rm HSP47}^{-}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 305.8; DB 22; Length 2526;
Pred. No. 7.3e-47;
0; Mismatches 257; Indels 51;
  55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2526 BP; 629 A; 653 C; 664 G; 580 T; 0 other;
  protein;
  protein interacting
                                                                                                                                                                                                                                                                                              KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 24; Page 21-22; 26pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.2%;
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Best Local Similarity 63.73
Matches 541; Conservative
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P-PSDB; AAG64212.
shock
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 AAACGAATCACCGCCTCCTAACCCGCGAAAAACCCCGGACCACCAATTACGCCCAA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279 CCCACGAAAAACCTCCCCTTAACGAACGACTTAAAAAACGACACGCGCGGGTAAAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGCGGGTCACCG-CTCCTGGCCCGCGGAGAGCCCCGGCCCCGGCAGCCATTGCGCCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 CCCTAAGAAACCAGCCGTCCGAGAAGCCGCGGATCTCAGGTGCCCAGGATCGTTAGGACT
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genome can be analyzed simultaneously and it is not essential he sequence context of all targeted regions. Primers may be defor preferential amplification of particular segments of
                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                 DB 22; Length 639;
                                                                                                                                                                                                                                      Indels
                                                                                                                                Sequence 639 BP; 80 A; 52 C; 196 G; 311 T; 0 other;
                                                                                                                                                                                                                                      0; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        661 GGCGCCGCCGTCGCAGTGCCATGGTGCTGCTGCTGCT
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                                                                                                                                                                                 Query Match 15.1%; Score 304.6; Best Local Similarity 69.3%; Pred. No. 1.16 Matches 443; Conservative 0; Mismatches
                                                                                   exons).
                                                                                   (e.g. promoters and
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                                                                                                                                                                                                  241 CCCGGGCCACCCGGCCCCATGGGGCCCCCGGGCGAGAAGGGCGAGCCCGGGCCGCCAAGGC 300
                                           ----GCTACGTGCCTCGCATTGCTTTCTACGCGGGCCTGCGGGGGCCCCACGAGGGTTAC
                                                                                                 -----CCACCAGGTCCAAGAGGGCCCCCAGGAGAACCCGGGCAGGCCCCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCAAGTTCACCTGCTCCATCCCGGGCATCTACTTCTTCACCTACCACGTCCTGATGCGC
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                         GGCGCCAAGGGAGAGGTGGGCCGGCGCGGAAAGCAGGCCTGCGGGGGGCCCCCTGGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide for detecting cytosine methylation SEQ ID NO 32363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCAACAAGTACAGCACCTTCTCCGGCTTCATCTACCCCCGACTGA 1399
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated polypeptide comprising a 277, 480, 881, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026, 844, 782, 262, 394, 471, 485, 286, 331, 495, 350, 691, 490, 462, 255, 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as given in the specification. The polypeptides, modulators of the polypeptides and antibodies against the polypeptides are useful for treating diseases such as neurological and psychiatric diseases including Alzheimer's, parasupranuclear palsy, Huntington's disease, myotonic dystrophy, anorexia and depression; cardiovascular disease, including congestive heart failure, Hoddkin's disease and myocardial infarction; respiratory diseases including asthma, chronic obstructive pulmonary disease, cystic fibrosis and adult respiratory distress syndrome; liver diseases including asthma, chronic obstructive pulmonary diseases including hypercholesterolaemia, cirrhosis, viral and nonviral hepatitis; Type II diabetes mellitis, and impalred glucose tolerance; renal disease including renal failure, acute tubular necrosis and glomerulonephritis; skeletal muscle diseases including diseases including testicular cancer, choraction; lymph diseases including testicular concerving the concerv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                683 ATGGTGCTGCTGCTGGTGGCCATCCCGCTGCTGGTGCACAGCTCCCGCGGGCCCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      743 CACTACGAGATGCTGGGTCGCTGCCGCATGGTGTGCGACCCGCATGGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----CCCCGTGGCCCTGGTCCCGACGCGCGCCTGCTTCCGTGCCCCCCTTCCCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   male reproductive diseases including low testosterone and male infertility; and disease of pancreas including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The present sequence encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                 Kabnick KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polypeptides and polynucleotides useful as a vaccine for preventing and treating diseases associated the polypeptide, e.g. Alzheimer's disease, dyslipidemia, obesity, diabetes, infertility,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 24; Length 768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 303.2; DB 24; Length
Pred. No. 2e-46;
0; Mismatches 208; Indels
                                                                                                                                                                                                                                                                                                                                               Smith RF, Xiang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 768 BP; 155 A; 259 C; 233 G; 121 T; 0 other;
                                                                                                                                                                                                                                                                                                                                               Murdock PR, Rizvi SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 61; 116pp; English.
                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide of the invention.
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                                                                                                                                                                                                          11-MAY-2000; 2000US-203336P.
25-MAY-2000; 2000US-207087P.
26-MAY-2000; 2000US-207546P.
                                                                                                                                                   26-APR-2001; 2001WO-US13360.
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P-PSDB; ABB53290.
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                                                                         WO200181363-A1
                                                                                                                                                                                                                                                                                                                                                               Xie Q;
                                       Homo sapiens.
                                                                                                                                                                                        27-APR-2000;
11-MAY-2000;
                                                                                                               01-NOV-2001
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ABQ45773 standard; DNA; 584

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methylation of a particular cytosine in a motif 5'CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (c) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonocleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54212 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the characterial and contracted the contracted and contracted
                                           agree of cytosine methylation in genomic DNA, useful
prognosis, comprises selective hybridization of
                                                                                                                                                                                                                                                                                             This invention describes a novel method for determining the degree of
                                                                                                                                                                                                              Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                           amplicons from chemically treated DNA
                                                degree
                                                                                   for diagnosis and
                                           Determining the
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Sequence 584 BP; 100 A; 45 C; 207 G; 232 T; 0 other;

the disclosure of the invention

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1512
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                                                                 1215 GACAGGTCCGGGCCAGCGCCATTGCTCAGGACGCGGACCAGAACTACGACTACGCCAGCA 1274
                                                                                                                           1275 ACAGCGTCATTCTGCACCTGGACGTGGGCGACGAGGTCTTCATCAAGCTGGACGGCGGGA 1334
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                                                                                   208 CCTTCCGTTCCCGTTAACGACCTAAATAAACGAACTCTTAATACTCAAAAATATAAAATAA
                                                                                                                                             387 AAATACACGACGACAACAAAATACAAAATACGACTTCTCCGACTT-ATCATACCC
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                                   Gaps
 Score 286.4; DB 24; Length 584;
Pred. No. 2.3e-43;
0; Mismatches 116; Indels 3;
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                 Best Local Similarity 76.6
Matches 389; Conservative
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> RESULT 7 ABQ45773 (

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methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic convert member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the contrained not promit the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the removal of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide cypes and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

ARDIALIO-ARGALIZI represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of
                                                                                                                                                            Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
drug; side effect; cancer; central nervous system; cardiovascular;
gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
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                                                                                                                       Oligonucleotide for detecting cytosine methylation SEQ ID NO 32364
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14.2%; Score 286.4; DB 24; Length 584;
Best Local Similarity 76.6%; Pred. No. 2.3e-43;
Matches 389; Conservative 0; Mismatches 116; Indels 3;
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05-SEP-2000; 2000DE-1044543
                                                                               (first entry)
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secreted polypeptide (I) and

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polynucleotide (II). (I) and (II) are useful for treating cancer, autoimmune diseases, wound healing disorder, infertions, haematopoietic disorders, inflammatory disorders, infertility, neurological and psychiatric diseases, cardiovascular diseases, respiratory diseases, rand diseases, or gastrointestinal diseases, These may also be used treat diseases, abnormalities and disorders caused by abnormal expression, production, function and/or metabolism of the genes, as creening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. The polypeptides can be used as immunogens to produce antibodies immunospecific for the polypeptides, and to identify membrane-bound or soluble receptors. The polypeptides, and to identify membrane-bound or soluble receptors. The polypeptides, and to identify membrane-bound or soluble receptors. The polypeptides, and in tissue expression studies. The present sequence represents the
                                                                                                                                                                                                                                                          Sequence 864 BP; 173 A; 271 C; 288 G; 132 T; 0 other;
                                                                                                                                                                                                                              coding sequence of novel human secreted protein #6.
                   invention relates to an isolated novel
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                                                                                   CCTTCCGTTCCCGGAGGCGGCCTAAATGGGCGAACTCTTGGTGCTCAAGGGTATAAGTGG 1572
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                                                                                                  CCGAAAAAAAAAAAACCCGACCAAAAAAAAAAAAAAGGACTTCCGAAAAAATCACCCGCA 496
                                                                                                                                                                                                                                                                      AAATACACGACGACAACAACAAATACAACACCTTCTCCGACTT-ATCATCTACCCCG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New secreted proteins or polypeptides, useful for treating e.g. cancer, autoimmune diseases, wound healing disorder, infections, haematopoietic disorders, inflammatory disorders, infertility, cancer
                                        Secreted protein; cytostatic; immunosuppressive; vulnerary; vaccine; antiinflammatory; neuroprotective; nephrotropic; cardiovascular; human; cancer; autoimmune disease; wound healing disorder; infection; heamatopoletic disorder; inflammatory disorder; infection; neurological disease; psychiatric disease; cardiovascular disease;
                             Smith RF, Xiang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Human secreted protein"
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                                                                                                                                                                                                                                                                                                                          DNA encoding novel secreted protein #6.
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                                                                                                                                                                                                                                                                                                                                                                                                            AAS17577 standard; cDNA; 864
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2000US-199417P
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24-APR-2000;
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       864;
Score 272.4; DB 24; Length
Pred. No. 8.4e-41;
0; Mismatches 176; Indels
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Query Match 13.5%;
Best Local Similarity 68.4%;
Matches 394; Conservative
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1215 GACAGGTCCGGGCCAGCGCCATTGCTCAGGACGCGGACCAGAACTACGACTACGCCAGCA 1274
238 CTCGCCACCCTCGTCCCCTCGTCTCCACTTTCAGGCTCAGGCTCCAG-CTTGGCAGCC 296
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(S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PSR). (I) comprising checked preferably by polymerase chain reaction (PSR). (I) comprising specific for an ovarian tumour protein comprising contexting T cells with (III) and/or (II) is useful for stimulating and/or expanding T cells with (III) or (III) is useful in design and preparation of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a ultable library e.g., a tumour cDNA library using well known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1846 CTGGCGCACCTCTGGTCCCCTCGTCTCCACTTTCAGGCTCAGGCTCCAGCCTTGGCAGCC 1905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention describes a composition (I) comprising: carriers
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                                                                                                                                                                                                                                                                                                                                                                           Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide .
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                                      Human; ovarian cancer; ovarian tumour; cytostatic; gene;
  Human ovarian cancer related cDNA clone SEQ ID NO:1219
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Pred. No. 3.4e-40;
0; Mismatches 5;
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96.8%;
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridisation to both classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue methylation status of many C residues to be determined simultaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method and a contraction of the decremination of the decreminati
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05-SEP-2000; 2000DE-1044543.
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Best Local Similarity 72.4
Matches 368; Conservative
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                                                               AAGTGCACGCGGCAACAACAACAAGTACAGCACCTTCTCCGGCTTCATCTTACCCCG 1394
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                                                                         TCCTGCCCCCCCCCCGAGGCGCCCACCCCATTGAGAGCCTGGCGGTGGGGTGGAC
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                          ACAGCGTCATTCTGCACCTGGACGTGGGCGACGAGGTCTTCATCAAGCTGGACGGCGGGA
                                                                                                                      octermining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA
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drug; side effect; cancer; central nervous system; cardiovascular;
gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
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05-SEP-2000; 2000DE-1044543.
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C to uracil, then part of the genomic convert a maphicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of the rapeutic drugs and of a wide range of diseases, each, despiratory systems etc., particularly by detecting mutations or single nucleotide cypes and for investigating cell differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. Appliation status of many C residues to be determined simultaneously.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate themethod for determining the degree of cytosine methylation described in the disclosure of the invention.
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72.4%;
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Matches 368; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1152 CTTACCACGTGCTCATGCGCGGGGGGGCACCAGCATGTGGGGCCGACCTCATGAAGA 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAGAGGGCCCCCAGGAGAACCCGGCAGGCCCCCCCGGGCCCTCCCGGTCCAGGTC 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a human Cig-related factor-like (CRF-like) protein, LP231, which has sequence homology to human cereballin, and its associated nucleic acid. The polypetides and polynucleotides are useful for treating or preventing neurological disorders associated with the inappropriate expression of cereballin-2 proteins and disruption of the synapse function, e.g. Parkinson's disease, Alzhahmer's disease, bipolar and unipolar affective disorders, schizophrenia, olivopontocereballar atrophy or Shy-brager syndrome. The nucleotide sequences (or their complements) have various applications in the art of molecular biology, including uses as hybridisation probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. This sequence represents CDNA encoding the human LP231 polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGACCAGTGCGCTGAGCGCCCACCTTCAGCGGCCCCAAGATCGCCTTCTATGTGGGGTCTCA
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                                 Human, CRF-like protein; LP231; Clq-related factor; gene; ss; cerebell neurological disorder; cerebellin-2; synapse function; schizophrenia; Parkinson's disease; Alzheimer's disease; bipolar affective disorder; unipolar affective disorder; olivopontocerebellar atrophy; nootropic; Shy-Drager syndrome; neuroprotective; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New LP231 polypeptides and polynucleotides, useful in gene therapy, particularly for treating or preventing neurological disorders, e.g. Parkinson's disease, Alzheimer's disease, schizophrenia or Shy-Drager
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 CCAGCGGCGTCGGGGTGGTGGCGCGCGGGGCTAGGTGGCGATTCCGAGGGTGAAG
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                                                                                                                                                                                                                                                 "Human LP231"
                                                                                                                                                                                           Location/Qualifiers
55..732
Human CRF-like protein LP231 cDNA.
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nes 344; Conservative
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-cpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to ureall, then part of the genomic cytosine (C) but not methylated C to ureall, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (11) for differentiation of cell or tissue
1271
                                                                                                                                                           1272 GCAACAGCGTCATTCTGCACCTGGACGTGGGCGACGAGGTCTTCATCAAGCTGGACGGCG 1331
                                                                                                                                                                                                                                                                                                                      1332 GGAAAGTGCACGGCGGCAACACCAACAAGTACAGCACCTTCTCCGGCTTCATCATCTACC 1391
                                                                                                                                                                                                                                    664
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                                                                                 545 ACGGGCAGGTCCGGGCCAGCGCCATTGCACAGGACGCCGACCAGAACTACGACTACGCCA
                                                                                                                                                                                                            Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA
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drug; side effect; cancer; central nervous system; cardiovascular;
gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide for detecting cytosine methylation SEQ ID NO 15913.
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2000DE-1044543.
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05-SEP-2000;
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1197 CCGACCTCATGAAGAACGGACAGGTCCGGGCCAGCGCCATTGCTCAGGACGCGGACCAGA 1256
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                                                                                                                                                                                                              462 CCTCCCGTATCCCCCACCCAAATACGAACCAATACTATTACCCAAAACGCGAACCAAA 403
                                                                                                                                                                                                                                                            methylation status of many C residues to be determined simultaneously. Mappla10.ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
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of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide for detecting cytosine methylation SEQ ID NO 15914.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA.
                                                                                                                        DB 24; Length 505;
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m The}
                                                                                      Sequence 505 BP; 81 A; 45 C; 222 G; 157 T; 0 other;
                                                                                                                       Score 107.6; DB 24;
Pred. No. 8.8e-11;
0; Mismatches 84;
 types and for investigating cell differentiation.
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                                                                                                                     Query Match 5.3%;
Best Local Similarity 65.3%;
Matches 158; Conservative
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Special Contains the target C is amplified to form a labeled amplicon. The amplicon is the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligonucleotides and/or peptide-nucleic acid (PNA) oligoners and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. Ampliation status of many C residues to be determined simultaneously.

The methylation determining the degree of cytosine methylation described in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism;
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                                                                                                                                                                                                                                                                                                                                                                                                           5.3%; Score 107.6; DB 24; Length 505; 65.3%; Pred. No. 8.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  84; Indels
                                                                                                                                                                                                                                                                                                                                                                      Sequence 505 BP; 157 A; 222 C; 45 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                               the disclosure of the invention,
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05-SEP-2000; 2000DE-1044543.
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(EPIG-) EPIGENOMICS AG

Guetig D; Berlin K, Piepenbrock C, Olek A,

WPI; 2002-371829/40.

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA

Claim 12; 56pp + Sequence Listing; 56pp; German.

methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine () but not methylated C, to uracil, then part of the genomic cytosine () but not methylated C, to uracil, then part of the genomic contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of the rapecutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

MB013410-AB054121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention. This invention describes a novel method for determining the degree of

Sequence 505 BP; 79 A; 45 C; 123 G; 258 T; 0 other;

ö DB 24; Length 505; 51; Indels 5.0%; Score 101.4; DB 2 72.1%; Pred. No. 1.2e-09; 0; Mismatches Best Local Similarity 72.1 Matches 132; Conservative Query Match

1218 AGGTCCGGGCCAGCGCCATTGCTCAGGACGCGGACCAGAACTACGACTACGCCAGCAACA 1277 셤

1278 GCGTCATTCTGCACCTGGACGTGGGCGACGAGGTCTTCATCAAGCTGGACGCGGGAAAG 1337

ò g 1338 TGCACGGCGCAACACCAACAAGTACAGCACCTTCTCCGGCTTCATCATCTACCCCGACT 1397 셤 ò

1398 GAG 1400

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Search completed: June Job time: 1344 secs

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Sequence 2, Ap
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
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Compugen Ltd
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1 US-09-103-840A-2

US-08-463-911-6

US-09-140-804-9

US-08-69-473-1

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US-09-231-818-1
US-09-411-687A-4
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US-09-197-649-7
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US-08-403-852D-3
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Maximum Match 100%
Listing first 45 summaries
                                                                  nucleic search, using.sw model
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Gapop 10.0 , Gapext 1.0
 GenCore (c) 1993
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length: 2000000000
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US-09-370-838-151

US-09-188-930-31

US-09-336-536-9

US-09-336-536-9

US-09-336-536-9

US-09-320-878-21

US-09-320-878-19

US-09-105-537-3

US-09-11-687A-24

US-09-411-687A-24

US-09-411-687A-24

US-09-411-687A-24

US-09-428-517-1

US-09-428-517-1

US-09-428-517-1

US-09-506-855-43

US-09-642-55-60
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                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09336536
Patent No. 6406884
GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: Leiby, K.
APPLICANT: Bossone, S.
FILE REFERENCE: 7853-144
CURRENT APPLICATION: SECRETED PROTEINS AND USE;
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
CURRENT FILING DATE: 1999-06-18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                       ALIGNMENTS
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Matches 369; Conservative
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49.4%; Pred. No. 5.6e-09;
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APPLICANT: Leiby, K.
APPLICANT: Merkay, C.
TITLE OF INVENTION: SECRETED PROTEINS AND USE
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT APPLICATION NUMBER: US/09/336,536
SOFTWARE OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 728
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Patent No. 6406884
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Pred. No. 3.6e-09;
0; Mismatches 370; Indels
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APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FASELSEQ for Windows Version 3.0
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Best Local Similarity 49.1%;
Matches 368; Conservative
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; LOCATION: (198)...(926)
US-09-140-804-1
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Patent No. 6265544
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
CURRENT APPLICATION NUMBER: US/09/118,408A
CURRENT APPLICATION NUMBER: 06/053,154
EARLIER APPLICATION NUMBER: 60/053,154
EARLIER APPLICATION NUMBER: 1997-07-18
MUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 47.5%;
Matches 291; Conservative
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; LOCATION: (171)...(1013)
US-09-118-408-1
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            CGGGGCTCCGGGAGAAAGGCGAGGCGGGAGCGGGACTGCCGGGACCTCGAGGGGAC 236
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APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
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CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 729
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Patent No. 6197930
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Sequence 1, Application US/09103840A
Setent No. 6224328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SOFTWARE: PATENTIN Ver. 2.1
                                                                                        1211 AACGGACAGGTCCGGGCCAGCGCCATTGCTCAGGACGCGGGACCAGAACTACGACTACGCC
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                                             522 TCAGCAGGGCCAGGGGCCACACTGGACCCAAAGGGCAGAGAGGGCTCCATGGGGGCCCCT
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CCAAGAGGGCCCCCAGGAGAACCCGGCAGGCCAGGCCCCCGGGCCCTCCCGGTCCAGGT
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44.1%; Pred. No. 0.00012;
tive 0; Mismatches 583;
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ORGANISM: Mycobacterium tuberculosis
OTHEN INFORMATION: H37Rv
US-09-103-840A-1
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                                          522 TCAGCAGGGCCAGGGCCACACACTGGACCCAAAGGGCAGAAGGGCTCCATGGGGGCCCCT
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Fatent No. 644821
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul O.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND
TITLE OF INVENTION: INMUNE FUNCTION
FILE REFERENCE: 99-12
CURRENT APPLICATION NUMBER: US/09/506,855
CURRENT APPLICATION NUMBER: 2000-02-17
NUMBER OF SEQ ID NOS: 50
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3.7%;
Best Local Similarity 47.5%;
Matches 291; Conservative
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US-09-506-855-1
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LENGTH: 2769
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US-09-506-855-1
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572 ATATGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGCTTCACCTATG 631

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1239 CTCAGGACGCGGACCAGAACTACGACTACGCCAGCAACAGCGTCATTCTGCACCTGGACG 1298
                                                                                               1399 TGGGCGACGAGGTCTTCATCAAGCTGGACGGCG------GGAAAGTGCACGGCGCGCA 1349
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                                                                                                                        415 TTCGCTTTACCAAGATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAAT
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                                                                                                                                                                                                   APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER RILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FASTSEQ for Windows Version 3.0
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Sequence 1, Application US/08690473
Sequence 1, S76923
GENERAL INFORMATION:
APPLICANT: Leopardt, Rosario
APPLICANT: Roliman Bernard
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 AS AN
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Pred. No. 0.00027
                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09140804 Patent No. 6197930 GENERAL INFORMATION:
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US-09-140-804-9
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1276 CAGCGTCATTCTGCACCTGGACGTGGGCGACGAGGTCTTCATCAAGCTGGACGGCGGGAA 1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08463911
Patent No. 586330
GENERAL INVERMATION:
APPLICANT: Scherer, Philipp E. APPLICANT: Lodish, Harvey F. ERUM PROTEIN PRODUCED TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,911
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0.0002;
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Pred. No. 0
                                                                                                                                                                                 REGISTRATION NUMBER: 32,27
REGISTRATION NUMBER: 32,27
REFENDE/DOCKET NUMBER: WH195-05
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-9540
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 1313 base_pairs
                                                                                                                                                          CTGAGCCGGCCCGCCCGTGC 1417
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
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Best Local Similarity 53.6'
Matches 186; Conservative
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EDNESS: single
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; LOCATION:
US-08-463-911-6
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COUNTRY:
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Sequence 1, Application US/09259821A Patent No. 6210926
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US-09-259-821A-1
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Best Local Similarity 47.6%;
Matches 245; Conservative
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                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                   GENERAL INFORMATION:
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                                         JS-09-259-821A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 61.8; DB 2; Length 4
Pred. No. 0.00032;
0; Mismatches 267; Indels
                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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TITLE OF INVENTION: INHIBITOR OF APOPTOSIS NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                            STATE: PLO. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                      REFERENCE DOCKET NUMBER: ARCD: 239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000.
TELEFAX: 512/4747
TELEFAX: 512/4747
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,473
FILING DATE: 26-VUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
3.1%;
Best Local Similarity 47.6%;
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4257 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                    MEDIUM TYPE:
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APPLICANT: LEOPARDI, ROSARIO
APPLICANT: ROIZMAN, BERNARD
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS
FILE REFERENCE: ARCD:317
CURRENT APPLICATION NUMBER: US/09/259,821A
CURRENT FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 08/690,473
PRIOR PELING DATE: 1996-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2631 CTCGGACGCCCGCGCCCCCCTCCCCGCGCCCCCCCCTCCACGCCCCCGGGGCCCGA 2690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 61.8; DB 4;
Pred. No. 0.00032;
0; Mismatches 267;
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Patent No. 6218103
GENERAL INFORMATION:
APPLICANT: Leopardl, Roasrio
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: HERPES SIMPLEX
NUMBER OF SEQUENCES: 6
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MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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US-08-458-568A-11/C
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Pred. No. 0.00032;
0; Mismatches 267; Indels
                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,659
FILING DATE: CONCULTENTLY HEYEWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: CONCULTENTLY HEREWITH CLASSIFTCHORY 435
ATORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DGOKET NUMBER: ARSB:519
TELECOMMUNICATION INFORMATION:
                                      Arnold, White & Durkee
                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4257 base pairs
                                                                                                                                                                 COUNTRY: United States 2IP: 77210
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Matches 245; Conservative
                                                                  : P.O. Box 4433
Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                            Texas
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RESULT 14

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Sequence 11, Application US/08458568A
Sequence 11, Application US/08458568A
Patent No. 5821339
GENERAL INFORMATION:
APPLICANT: Schaffer, Priscilla A.
APPLICANT: Yeh, Lily.
TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus
TITLE OF INVENTION: Infections
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION 1943:

PRIOR APPLICATION 1943:

APPLICATION NUMBER: US 08/065,146
FILING DATE: 05-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn R.
REGISTATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: DECI-0029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Herpes simplex virus
; STRAIN: Herpes Simplex Virus Type 1
US-08-458-568a-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/458,568A FILING DATE: 02-JUNE-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
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                                                                                           4044
                                                                                                                                          163 CGCCGCCTCCGCCGCGCGCGCGCGCGCCAAGCGCAAGAGTCCCGGCCCGGCCCGGCC 4104
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TGCCGCATGGTGTGCGACCCGCATGGGCCCCGTGGCCCTGGTCCCGACGGCGCGCCTGCT
                                                          TCCGTGCCCCCCTTCCCGCCAGGCGCCAAGGGAGGTGGGCCGGCGCGGGAAAGCAGGC
                                                                                         1103 GCCCGGAGGCGGCGCCCCCCGCAACCCAAGAAGAAGAGGCGCGCGCGCACGCCCCGG
                                                                                                                      CTGCGGGGGCCCCCTGGACCACCAGGTCCAAGAGGGCCCCCCAGGAGAACCCGGCAGGCCA
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Pred. No. 0.0025;
0; Mismatches 572; Indels
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: WHITE, OWER R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENEER, Claire M.
APPLICANT: VENEER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
TILLE OF INVENTION: TUBERCULOSIS
TILLE OF INVENTION: TUBERCULOSIS
CURRENT APPLICATION WUBBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 2
                                                                                                                                                                                                       GCCCCCCCGGCCCTCCCGGTCCAGGTCCGGGCGG 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09103840A
Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
3.0%;
Best Local Similarity 43.8%;
Matches 455; Conservative (
                                                                                                                                                                                                                                                                                                              Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, RODERT
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OTHER INFORMATION: C
OTHER INFORMATION: "
OTHER INFORMATION: r
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US-09-103-840A-2/C
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3927898 GGCCCAGGCCGAGACCGCTGGCTCCCTCGCCGCCGTCACCGCCAACACCGCCGTTTCCGC 3927839
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3928310 GCTAGCCCGGTGCTGTTCAGGCCGCCTTTGCCGCCTTGGCCGCCGTGGCCGCCGCGCACCA 3928251
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                                                              CGTGCCCCCCTTCCCGCCAGGCGCAAGGGAGAGGTGGGCCGGGCGCGGGAAAGCAGCCTT
                                                                                                                                              GCGGGGCCCCCTGGACCACCAGGTCCAAGAGGGCCCCCAGGAGAACCCGGCAGGCCAGG
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Search completed: June 6, 2003, 20:55:23 Job time : 136 secs

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1725
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Patent No. US2002013237A1

GENERAL INFORMATION:

APPLICANT: Aglate, Paul A.

APPLICANT: Jones, Robert

APPLICANT: Harlocker, Susan L.

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.497

CURRENT PILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 466;
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96.8%; Pred. No. 6.8e-61;
iive 0; Mismatches 5;
             US-10-140-470-361
US-10-176-918-361
US-10-176-921-361
US-10-176-921-361
US-10-176-921-361
US-10-140-474-361
US-10-140-474-361
US-10-140-474-361
US-10-142-419-361
US-10-142-419-361
US-10-142-42-361
US-10-121-050-361
US-10-121-050-361
US-10-121-050-361
US-10-121-050-361
US-10-123-262-361
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US-10-123-262-361
US-10-123-262-361
US-10-123-262-361
US-10-123-262-361
US-10-123-262-361
US-10-123-262-361
US-10-123-262-361
US-10-123-292-361
US-10-123-292-361
US-10-123-292-361
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US-10-123-292-361
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LCCATION: (1)...(466)
CTHER INFORMATION: n = A,T,C or G
US-09-867-701-1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity 96.8
338; Conservative
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Query Match
Best Local S.
Matches 338
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Sequence 1, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1671, Ap
Sequence 1671, Ap
Sequence 182, App
Sequence 182, App
Sequence 67, Appli
Sequence 67, Appli
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                                                                                                                                                                (without alignments)
9160.608 Million cell updates/sec
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1. /cgn2_6/ptodatta/2/pubpna/US07_PUBCOMB.seq:*
2. /cgn2_6/ptodatta/2/pubpna/PCT_WINE_PUB.seq:*
3. /cgn2_6/ptodatta/2/pubpna/PCT_WINE_PUB.seq:*
4. /cgn2_6/ptodatta/2/pubpna/US06_NEW_PUB.seq:*
5. /cgn2_6/ptodatta/2/pubpna/US06_PUBCOMB.seq:*
6. /cgn2_6/ptodatta/2/pubpna/US08_NEW_PUB.seq:*
7. /cgn2_6/ptodatta/2/pubpna/US08_PUBCOMB.seq:*
8. /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9. /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10. /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
11. /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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11. /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
11. /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
                                                                                                                                       6, 2003, 20:04:08; Search time 308 Seconds
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-764-872-823
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US-10-098-841-182
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US-09-796-753-67
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US-10-121-049-361
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US-09-998-563-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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912 CAAGAGGCCCCCAGGAGAACCCGGCAGGCCCCCCGGGCCCTCCCGGTCCAGGTC
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                                                                                                    Length 795;
                                                                                                                                                                            Sequence 1, Application US/09998563

Patent No. US20020155546A1

GENERAL INFORMATION:

APPLICANT: Fox, Brian

TITLE OF INVENTION: ADIPOCYTE COMPLEMENT RELATED PROTEIN

TITLE OF INVENTION: ACRP12

FILE REFERENCE: 00-93

CURRENT APPLICATION NUMBER: US/09/998,563

CURRENT FILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-11-29

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASTSEQ for Windows Version 3.0
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Pred. No. 3.4e-
0; Mismatches
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Best Local Similarity 70.9%;
Matches 343; Conservative (
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (46)...(795)
US-09-998-563-1
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LENGTH: 795
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                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Degenerate polynucleotide encoding a propertion of SEQ ID NO:2
NAME/KEY: variation
LOCATION: (1)...(750)
NAME/KEY: misc_feature
LOCATION: (1)...(750)
OTHER INFORMATION: n = A,T,C or G
UCHER INFORMATION: n = A,T,C or G
                                                                   APPLICANT: FOX. Brian
TITLE OF INVENTION: ADIPOCYTE COMPLEMENT RELATED PROTEIN
TITLE OF INVENTION: ZACRP12
FILE REFERENCE: 00-93
FURENT APPLICATION NUMBER: US/09/998,563
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 60/253,867
NUMBER OF SD ID NOS: 4
SOFTWARE: FASTERQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.8%; Score 237.8; DB 9; Best Local Similarity 52.0%; Pred. No. 1e-52; Matches 213; Conservative 85; Mismatches 112;
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PATENT NO. USZ0020106474A1
CENERAL INFORMATION:
APPLICANT: Fox, Brian
Sequence 3, Application US/09998563
Patent No. US20020155546Al
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                               49;
                                                                                                                                                                                                                                      DB 9; Length 804;
                                                                                                                                                                                                                                    Score 181.4; DB 9; Length 8 Pred. No. 5.9e-38; 0; Mismatches 236; Indels
TITLE OF INVENTION: ADIPOCYTE COMPLEMENT RELATED PROTEIN TITLE OF INVENTION: ZACRP11 FILE REFERENCE: 00-91
                                   CURRENT APPLICATION NUMBER: US/09/998,582
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 60/253,863
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 804
                                                                                                                                                                                                                                     9.0%;
                                                                                                                                                                                                                                  Query Match 9.0
Best Local Similarity 60.3
Matches 432; Conservative
                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (1)...(804)
US-09-998-582-1
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RESULT 5 US-09-998-582-3

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1043 GAGGGTTACGAGGTGCTGCGCTTCGACGACGTGGTGACCAACGTGGGCAACGCCTACGAG 1102
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                                                                      APPLICANT: FOX, Brian
TITLE OF INVENTION: ADIPOCYTE COMPLEMENT RELATED PROTEIN
TITLE OF INVENTION: ZACRP11
FILE REPERENCE: 00-91
CURRENT APPLICATION NUMBER: US/09/998,582
PRIOR APPLICATION NUMBER: US/09/253,863
PRIOR PILING DATE: 2000-11-29
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                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
Sequence 3, Application US/09998582
Patent No. US20020160474A1
GENERAL INFORMATION:
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OTHER INFORMATION: n = A,T,C or G
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LENGTH: 804
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1187 AGCATGTGGGCCGACCTCATGAAGAACGGACAGGTCCGGGCCAGCGCCATTGCTCAGGAC 1246
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   608 GAAAAGGTGATCACCAATGTTAATGATAACTACGAGCCGCGCAGTGGCAAGTTCACCTGC
                                                                                                                  728 AACATCGTGCGCGGCGGCGGACCGAGACGCAGGAAGTTCTCACCTTCTGCGACTAT
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Publication No. US20030050231A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA125

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper; NUMBER OF SEQ ID NOS: 957

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 823

LENGTH: 15558
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73.4%; Pred. No. 3.1e-15;
tive 0; Mismatches 48;
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US-09-764-872-823/c
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US-09-864-761-11941
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                                                                                                          4.9%; Score 98.2; DB 10; Length 46.9%; Pred. No. 3.5e-16; Live 0; Mismatches 348; Indels
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APPLICANT: Porter, Mark
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: MOLECULAT TOXICOLOGY MODELING
FILE REPERBREE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2000-11-02
PRIOR PELICATION NUMBER: US 60/290,029
PRIOR PELICATION NUMBER: US 60/290,029
PRIOR PELICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 2001-06-06
PRIOR PRIOR PELICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-19
PRIOR PELICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-19
PRIOR PELING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/298,884
PROR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/298,884
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PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR PRIOR PILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR PRIOR PILING DATE: 2001-06-19
PRIOR PRIOR PILING DATE: 2001-06-19
PRIOR PILING DATE: 2001-06-19
PRIOR PELING DATE: 2001-07-09
NUMBER OF SEO ID NOS: 1140
SSOFTHARE: PALEARLIN VET. 2.1
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Patent No. US20020119462A1
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ORGANISM: Rattus norvegicus
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Best Local Similarity 46.99
Matches 307; Conservative
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LENGTH: 1136
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992 GCCGGCTACGTGCCTCGCATTGCTTTCTACGCGGGCCTGCGGCGCCCCACGAGGGTTAC 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                           365 GGGAACCTGTGCGTGAACCTCATGCGTGGCC-----GGGAGCGTGCACAAGGTGGTC
                                                                                                            185 GCCACCCAGAAATCGCCTTCTGGCCACAAAAACCATCAACGTCCCCCTGCGCGGGAC
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TITLE OF INVENTION: No. US20020197679Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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CURRENT APPLICATION NUMBER: US/10/098,841
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 09/598,042
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR PELING DATE: 2000-04-25
PRIOR PELING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 182, Application US/10098841 Publication No. US20020197679A1 GENERAL INFORMATION:
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SOFTWARE: PLFL_genes Version 1.0
SEQ ID NO 182
LENGTH: 1185
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Qian, Xiaohong B
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Ma, Yunqing
Wang, Jian-Rui
Zhao, Qing A.
Ren, Feiyan
Chen, Rui-hong
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APPLICANT: Liu, Chenghua
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Xu, Chongjun
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ORGANISM: Homo sapiens
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LOCATION: (165)..(926)
US-10-098-841-182
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    872 GGGAAAGCAGGCCTGCGGGGCCCCCTGGACCACCAGGTCCAAGAGGCCCCCAGGAGAA 931
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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Pred. No. 6.6e-15;
0; Mismatches 293;
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PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-30
                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
                                                                                                                               FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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LIOR FILING DATE: 2001-01-30
KIOR PLICATION NUMBER: PCT/USO1/00668
KIOR FILING DATE: 2001-01-30
KIOR PPLICATION NUMBER: PCT/USO1/00663
KIOR FILING DATE: 2001-01-30
KIOR PPLICATION NUMBER: PCT/USO1/00663
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                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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Best Local Similarity 48.8%;
Matches 285; Conservative
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LENGTH: 600
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1023 CGGGCCTGCGGCGCCCCCACGAGGGTTACGAGGTGCTGCGCCTTCGACGACGTGGTGACCA 1082
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                                                                               268 ccoscitoscocoacradacaacaacaacaacaacocreiscocosococosococosoco
                                                                                                                                                                                                                                        208 GGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGCTGCTCCTGGGCCTGGCGG 267
                                                                                                                                                                   783 CGCATGGGCCCCGTGGCCCTGGTCCCGACGCGCGCCTGCTTCCGTGCCCCCTTCCCGC
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                                          723 ACAGCTCCCGCGGGCCAGCGCACTACGAGATGCTGGGTCGCTGCCGCATGGTGTGCGACC
                                                                                                                                                                                                              843 CAGGCGCCAAGGGAGAGGTGGGCCGGCGGGGAAAGCAGGCTGCGGGGGCCCCCTGGAC
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TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR PLING DATE: 1999-02-26
PRIOR PLING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
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Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENEE DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT PILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                               1127 CCCATGCCAGGCGTCTACTTCGCTTACCACGTGCTCATGCGCGGCGGCGACGGCACC 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCATGTGGGCCGACCTCATGAAGAACGCACAGGTCCGGGCCAGCGCCATTGCTCAGGAC 1246
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                                                                                                                                                                                                                               CCTGGGAATCCAGGAAAAGTCGGCCCCAAGGGCCCCATGGGCCCTAAAGGTGGCCCAGGG 470
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                                                                                                                                           GGGCTTCCAGGGCTGGCTGGAGACCATGGTGAGTTCGGAGAGAAGGGAGACCCAGGGATT
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                                                              Gaps
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19.4%; Pred. No. 1.5e-13;
ve 0; Mismatches 368; Indels 11;
                                                              ;
9
                      Length 1185;
                 Score 91; DB 9; Length 118
Pred. No. 2.7e-14;
0; Mismatches 285; Indels
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; OTHER INFORMATION: Incyte ID No. US20020137081A1 034470.4
US-10-044-090-60
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Matches 370; Conservative
                                     al Similarity 48.9
278; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 1377
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                 Query Match
Best Local S
Matches 278
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1083 ACGTGGGCAACGCCTACGAGGCAGCCAGCGGCAAGTTTACTTGCCCCATGCCAGGCGTCT 1142
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                                                                     523 AGC----CGGGTGCCTCCGCGTCTGACGCACCCTTCGACCGCGTGCTGGTGA 577
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  464 GGCC-TGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCCAAGCGCTCCGAG 522
                                                                                                                                                           1023 CGGGCCTGCGGCGCCCCCACGAGGGTTACGAGGTGCTGCGCGTTCGACGACGTGGTGACCA
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FILE REFERENCE: P2544PIC1
CURRENT APPLICATION NUMBER: U5/09/944,413
CURRENT FILING DATE: 2001-09-26
PRIOR PPLICATION NUMBER: 09/866,028
PRIOR PPLICATION NUMBER: 06/067,411
PRIOR PPLICATION NUMBER: 06/067,411
PRIOR PLLING DATE: December 1, 1997
PRIOR PLLING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
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FILING DATE: December 12, 1997
APPLICATION NUMBER: 60/069,696
FILING DATE: December 16, 1997
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Patent No. US20020156004A1
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Filvaroff, Ellen
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Botstein, David
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Goddard, Audrey
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Roy, Margaret
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Pred. No. 5e-13;
0; Mismatches 368;
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R APPLICATION NUMBER: 09/409,634

R FILING DATE: 1999-09-30

R FILING DATE: 1999-12-23

R APPLICATION NUMBER: 09/471,179

R APPLICATION NUMBER: 09/474,071
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PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR FILING DATE: 2000-06-29
                                         09/336,536
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09/312,359
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FILING DATE: 1999-06-30
APPLICATION NUMBER: 09/3
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FILING DATE: 2000-06-19
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FILING DATE: 2000-06-22
APPLICATION NUMBER: 09/6
                                                                                                        1999-06-29
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                       1999-05-1
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Best Local Similarity 49.39
Matches 369; Conservative
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PRIOR FILING DATE: 2000-05
NUMBER OF SEQ ID NOS: 162
                                     APPLICATION NUMBER:
FILING DATE: 1999-00
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APPLICATION NUMBER:
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FILING DATE: 2000-0
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                                                                                        APPLICATION NUMBER:
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PRIOR FILING DATE: 2000-0
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; ORGANISM: Homo sapiens
US-09-796-753-67
                                                                                                          FILING DATE:
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1023 CGGGCCTGCGGCGCCCCACGAGGTTACGAGGTGCTGCGCTTCGACGACGTGGTGACA 1082
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                                                                                                                                                                                                                                                                                                                                                678 ACTACTTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGA 737
                                                                                                             267 CCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGCCCGGGGCACCCCGGGCC 326
                                                                                                                                                                                                                                327 TTCCAGGCACGCCGGGCC---ACCATGCCAGGGCTTGCCGGGCCGCGCGATGCCGCG 383
                                                                                                                                                                                                                                                                                         843 CAGGCGCCAAGGGAGAGGTGGGCCGGCGGGAAAGCAGGCCTGCGGGGGCCCCCTGGAC 902
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Patent No. US20020165143A1
GENERAL INFORMATION:
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Grimaldi, Christopher
Gurney, Austin
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APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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Napier, Mary
Roy, Margaret
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4.2%; Score 85; DB 9; Length 1377;
Best Local Similarity 49.1%; Pred. No. 1e-12;
Matches 368; Conservative 0; Mismatches 370; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IOR APPLICATION NUMBER: 60/146, 22

IOR FILING DATE: July 28, 1998

IOR APPLICATION NUMBER: PCT/0598/1930

IOR APPLICATION NUMBER: PCT/0598/1930

IOR APPLICATION NUMBER: PCT/0598/25108

IOR FILING DATE: September 16, 1998

IOR APPLICATION NUMBER: PCT/0598/25108

IOR APPLICATION NUMBER: 09/216, 021

IOR FILING DATE: December 16, 1998

IOR APPLICATION NUMBER: 09/254, 311

IOR FILING DATE: March 3, 1999

IOR APPLICATION NUMBER: PCT/0599/21090

IOR FILING DATE: September 15, 1999

IOR APPLICATION NUMBER: PCT/0599/28409

IOR APPLICATION NUMBER: PCT/0599/28313

IOR APPLICATION NUMBER: PCT/0599/283101
                                          PRIOR APPLICATION NUMBER: 60/069,870
PRIOR PELICATION NUMBER: 60/069,873
PRIOR PELICATION NUMBER: 60/069,873
PRIOR PELICATION NUMBER: 60/074,1097
PRIOR PELICATION NUMBER: 60/074,1096
PRIOR PELICATION NUMBER: 60/113,296
PRIOR PELICATION NUMBER: 90/218,119
PRIOR PELICATION NUMBER: PCT/US99/28013
PRIOR PELICATION NUMBER: PCT/US99/28019
PRIOR PELICATION NUMBER: PCT/US99/28019
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PRIOR APPLICATION NUMBER: PCT/US09/28019
PRIOR PELICATION NUMBER: PCT/US09/28019
PRIOR PE
               R FILING DATE: December 16, 1997
R APPLICATION NUMBER: 60/069,870
R APPLICATION NUMBER: 60/069,870
R APPLICATION NUMBER: 60/069,873
R FILING DATE: December 17, 1997
R APPLICATION NUMBER: 60/068,017
R APPLICATION NUMBER: 60/070,440
R FILING DATE: December 18, 1997
R FILING DATE: FEBRUARY 5, 1998
R APPLICATION NUMBER: 60/074,095
R FILING DATE: FEBRUARY 9, 1998
R APPLICATION NUMBER: 60/074,095
R FILING DATE: FEBRUARY 9, 1998
R APPLICATION NUMBER: 60/074,095
R FILING DATE: FEBRUARY 25, 1998
R APPLICATION NUMBER: 60/074,095
R FILING DATE: FEBRUARY 25, 1998
R APPLICATION NUMBER: 60/112,850
R FILING DATE: December 16, 1998
R APPLICATION NUMBER: 60/113,296
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; ORGANISM: Homo Sapien
US-09-944-413-41
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INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

Wood, William

APPLICANT: TITLE OF I

ŝ 963 GTCCAGGTCCGGGCGGGGGGGCGCCCGCTGCCGATGCTTTCTACG 1022 1023 CGGCCTGCGGCGCCCCACGAGGTTACGAGGTGCTGCGCTTCGACGACGTGGTGACCA 1082 1083 ACGTGGGCAACGCCTACGAGGCAGCCAGCGAAGTTTACTTGCCCCATGCCAGGCGTCT 1142 1262 GACTACGCCAGCAACAGCGTCATTCTGCACCTGGACGTGGGCGACGAGGTCTTCATCAAG 1321 1143 ACTICITCGCTTACCACGTGCTCATGCGCGGCGGC-GACGGCACCAGCATGTGGGCCGAC 1201 .202 CTCATGAAGAACGGACAGGTCCGGGCCAGCGCCATTGCTCAGGACGCGGGACCAGAACTAC 1261 842 443 266 782 327 TTCCAGGCACGCCCGGCC---ACCATGCCAGGCCTTGCCGGGCCGCGCGATGCCCGCG 383 843 CAGGCGCCAAGGGAGAGGTGGGCCGGCGGGAAAGCAGGCCTGCGGGGGCCCCCTGGAC 902 504 GGCC-TGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTCCGAG 562 207 GGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGCTCCTGGCCTGGCGG 267 CCGGCTCGCCCCCACTGGACGAGATCCCCAGCCTCTGCCCGGGGCACCCGGGC 783 CGCATGGGCCCCGTGGCCCTGGTCCCGACGGCGCGCCTGCTTCCGTGCCCCCTTCCCGC 663 GCGCGCCGTCGCAGGTGCCTGCTGCTGCTGCTGCTGCTCCCGCTGCTGCTGGTGC 723 ACAGCTCCCGCGGGCCAGCGCACTACGAGATGCTGGGTCGCTGCCGCATGGTGTGCGACC 903 CACCAGGTCCAAGAGGCCCCCCAGGAGAACCCGGCAGGCCAGGCCCCCGGGCCCTCCCG 563 AGC-----CGGGTGCCTCCGCCGTCTGACGCACCCCTTGCCCTTCGACCGCGTGCTGGTGA 797 CTCTCGGGGGGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGT Gaps 11; 4.2%; Score 85; DB 9; Length 1377; 49.1%; Pred. No. 1e-12; 0; Mismatches 370; 1382 ATCATCTACCCGACTGAGCCGGCCCCGC 1410 PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION UNMER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: PEDRIOR POT/US01/06520
PRIOR FILING DATE: FEBRUARY 28, 2001
NUMBER OF SEQ ID NOS: 120 Best Local Similarity 49.1 Matches 368; Conservative ; TYPE: DNA ; ORGANISM: Homo Sapien US-09-944-403-41 LENGTH: 1377 SEQ ID NO 41 849 Query Match 윤 õ g δ g ò 셤 g ò g ò 셤 g à g à ò ò Q δ qq à

US-09-944-896-41

RESULT 14

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1143 ACTICITCGCTTACCACGTGCTCATGCGCGGGGC-GACGGCACCAGCATGTGGGCCGAC 1201
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                                       APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020168715Atamber 30,
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020168715A1ember 30,
                                                                                  PRIOR FILING DATE: No. US20021089/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28311
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December1, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR PLICATION NUMBER: PCT/US00/03565
PRIOR APPLICATION NUMBER: PCT/US00/03665
PRIOR PLING DATE: February 11, 2000
PRIOR PLING DATE: February 22, 2000
PRIOR PLING DATE: February 22, 2000
PRIOR PLING DATE: PEDTUARY 22, 2000
PRIOR PLING DATE: March 2, 2000
PRIOR PLING DATE: March 3, 2000
PRIOR PLING DATE: March 30, 2000
PRIOR PLING DATE: May 22, 2000
PRIOR PELING DATE: MAY 22, 2000
PRIOR PLING DATE: MAY 22, 2000
PRIOR PLING DATE: JULY 28, 2000
PRIOR PLING DATE: JULY 28, 2000
PRIOR PLING DATE: JULY 28, 2000
PRIOR PLING DATE: DATE: PCT/US00/2670
PRIOR PLING DATE: DATE: PCT/US00/2650
PRIOR PLING DATE: PCT/US01/06520
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Best Local Similarity 49.1%;
Matches 368; Conservative 0
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ORGANISM: Homo Sapien
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TILE REFERENCE: P2546PIC1

CURRENT APPLICATION NUMBER: US/09/944,896

CURRENT FILING DATE: 2001-08-31

PRIOR PELICATION NUMBER: 09/866,028

PRIOR PELLING DATE: 2001-05-25

PRIOR PELLING DATE: 2001-05-25

PRIOR PELLING DATE: DOCEMBER 11, 1997

PRIOR PELLING DATE: DECEMBER 12, 1997

PRIOR PELLING DATE: DECEMBER 12, 1997

PRIOR PELLING DATE: DECEMBER 16, 1997

PRIOR APPLICATION NUMBER: 60/069,813

PRIOR PELLING DATE: DECEMBER 16, 1997

PRIOR APPLICATION NUMBER: 60/069,813

PRIOR PELLING DATE: DECEMBER 17, 1997

PRIOR APPLICATION NUMBER: 60/069,813

PRIOR PELLING DATE: DECEMBER 17, 1997

PRIOR PELLING DATE: DECEMBER 17, 1997

PRIOR APPLICATION NUMBER: 60/069,813

PRIOR PELLING DATE: DECEMBER 17, 1997

PRIOR APPLICATION NUMBER: 60/074,086

PRIOR PELLING DATE: JOHNARY 5, 1998

PRIOR PELLING DATE: FEBRUARY 9, 1998

PRIOR PELLING DATE: FEBRUARY 9, 1998

PRIOR PELLING DATE: PECTUARY 9, 1998

PRIOR PELLING DATE: PEDCEMBER 16, 1999

PRIOR PELLING DATE: DECEMBER 109/218, 311

PRIOR PELLING DATE: DATE:
Sequence 41, Application US/09944896
Patent No. US20020168715A1
                                                                                                                                                                                                                                                                                                                                                           Grimaldi,Christopher
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Filvaroff, Ellen
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Hillan, Kenneth
                                                                                                                            Botstein, David
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                                                                                               APPLICANT: Baker, Kevin
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                                                       1262 GACTACGCCAGCAACAGCGTCATTCTGCACCTGGACGTGGGCGACGACGTCTTCATCAAG 1321
797 CTCTCGGGGGGGCCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGT
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
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APPLICATION NUMBER: 60/068,01
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Patent No. US20020173463A1
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APPLICATION NUMBER: 60/069,87
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Botstein, David
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FILING DATE: Decembe
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0; Mismatches 370; Indels
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APPLICATION NUMBER: PCT/0S99/28409
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APPLICAN NUMBER: PCT/US99/28313
APPLICAN DATE: No. US20020173463Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR PELICATION NUMBER: 60/113, 296
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PRIOR APPLICATION NUMBER: PCT/US00/06419
PRIOR PELING DATE: PEDEUARY 22, 2000
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Best Local Similarity 49.1%;
Matches 368; Conservative
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AL561826 LTL_NFL004_NBC2 Homo sapiens CDNA clone CSODBOO5YK05 3
prime, mRNA sequence.

AL561826

AL561826.1 GI:12909642
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1 (bases 1 to 967)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Evil-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EWRY cedex - France

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Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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TITLE
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AL529897 AL529897
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
                                             nucleic search, using sw model
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Catarrhini; Hominidae; Homo.
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                                                                                  1955 CATICTGTACAGTCCCCATICCCCCCTATCCGGACTAGGCCCTGGGGCTACAGCTGCTGC
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                          123 CCTTGCCAGCCTTCCTGTGAACTGGAGGAACCAGTGAATTCTTTCCTGGCATTAAAACG
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E 1 (bases 1 to 914)

L (bases 1 to 914)

Contact: Gruber,C., Jessee,J. and Polayes,D.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segrefégenoscope.cns.fr.

Location/Qualifiers

Location/Qualifiers
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) priner. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RW sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies. Contact: Feng Liang Life Technologies. Ontact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center B371 Email: filang@lifetech.com URL: http://fulling@lifetech.com URL: at 179 200 t 2 others
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Matches 959; Conservative
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/clone="Lib="LTI_NFL004_NBC2"
/sax="male"
/tissue_type="neuroblastoma cells"
/lab_host="blub"
/lab_host="blub"
/note="Organ: brain; Vector: pcMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco NV sites of the pcMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Context: Feng Ling Ling
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Emall: fillang@ilfetech.com URL:
http://fulllength.invitrogen.com"
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Mammalla: Eutheria: Primates: Catarrhini; Hominidae; Homo.

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S Li,Wab. Gruber.C., Jessee.J. and Polayes,D.

Eul.-Inength cDNA libraries and normalization

I Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

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BP 191 91006 EVRY cedex - France

BM 191 92006 EVRY cedex - France

BM 191 92006 LOST CONTACT - CON
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 AACTACGACTACGCCAGCAACAGCGTCATTCTGCACCTGGACGTGGGCGACGAGGTCTTC
                                       ATCAAGCTGGACGCGGGAAAGTGCACGGCGGCAACAACAAGTACAGCACCTTCTCC
                                                        TCCCGTCCTCACCCACCTCCTGCCCGCCCCCAGGCGCCCACCCCACCCTTTGAGAGC
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Length
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Score 869.8; DB 9;
Pred. No. 2.9e-163;
9; Mismatches 6;
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503 480 563

323 300 383 360 443 540

623 909 683 999 743 720 803

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894 bp mRNA linear EST 13-FEB-2001
Homo sapiens cDNA clone CS0DA009YF06 5
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 894)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Pull-length cDNA libraries and normalization

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRX cedex - France
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                                                                                                                                            324 AGAAGCCGCGGGATCTCAGGTGCCCAGGATCGTTAGGACTGAACGGGAGGGTACTAGAGGA
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                                                                                CCTGAGAGAGCAGTCTGGAGAGCAGCATCTCAGATCCCTAAGAAACCAGCCGTCCG
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Prime, mRNA sequence.
AL518440 AL518440.1 GI:12781933
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/lab_host="neuroblastoma cells"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : filangelifetech.com URL :
http://fullneghh.invitrogen.com"
60 a 307 c 357 g 112 t 6 others
                                                CCATAGGGGCAGAGGTCGTGGCTTTCTCTTTTGTACAGAGATGGGGAGCAGTTTTAATAG 1711
                                                                                                            CGGGACTCAGAGGCCCAGAAGCCGGAGGGAAGCCCCCGCAGCTTGCGAGGGAAATAACA 1771
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 942)
24 GGACCGCCCCCCCAGAGAGAGGCGCGGGCCAGGGCTACTAGCAGGGACTGGGGCCGCGGG
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqreféqenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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98.8%; Pred. No. 4.9e-163;
tive 5; Mismatches 4;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODD005YH17"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
                                                                                                                                                                             GAAACAGGAGGAGCCCATT 1790
                                                                                                                                                                                            GAAACAGGAGGRGCCATT 917
                                                                                                                                                                                                                                                                                                                      prime, mRNA sequence.
AL529898
AL529898.1 GI:12793391
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/issue_type="neuroblastoma cells"
//lab_host="DH10B"
//lab_host="DH10B"
//lab_host="DH10B"
//note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and coloned into the Not I and Eco RV sites of the pcWNSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville illang@ilfetech.com URL:
                                                                                                                                                                                                                                                                      AL518439 LTI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA009YF06 3
Prime, mRNA sequence.
AL518439.1 GI:12781932
EST.
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                                                                    CCCGCATGGGCCCCGTGGCCCTG-GTCCCGACGCCGCGCGCTTCCGTGCCCCCTTCC 839
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 870)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                   CGCCAGGCGCCAAGGGAGAGGTGGGCCGCGCGCGGAAAGCAGGCCTGCGGGGGCCCC 896
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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241 c 301 g 163 t 1
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Pred. No. 2.6e-154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/clone_lib="LTI_NFL011_NBC1"
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/lab.host="DH10B"
/note="Organ: brain, Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library is not normalized, but is the control for
the normalized libraries. Library was constructed by Life
Technologies. Contact : Feng Liang Light Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
inversitation of Landing CONFO, USA Fax : (1) 301 610 8371 Email :
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segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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fliang@lifetech.com URL :
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8; Mismatches 2;
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/sex="male"
                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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1 (bases 1 to 557)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
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Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCCGCAGAGGCAGGGTAAGGGGAACC-GGGGGGCCAGCCGTCGGGGGAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.8%; Score 479.8; DB 14; 98.9%; Pred. No. 1.3e-85; tive 0; Mismatches 2;
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                                                                                                                                                                                                                                                       /organism="Homo sapiens"
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Emal: yongsung@mail.kribb.re.kr
Plate: 11 row: G column: 04
High quality sequence stop: 557.
Location/Qualiflers
                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
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160 c
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Best Local Similarity 98.9
Matches 525; Conservative
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160 g
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96.2%;
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119 c
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Best Local Similarity 96.2
Matches 384; Conservative
                                                                                    mRNA sequence.
BM844470
                                                                                                                                                                     Homo sapiens
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ORIGIN
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                                                                                                                   VERSION
KEYWORDS
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                    RESULT 9
BM844470
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                                BE888168 387 bp mRNA linear EST 20-OCT-2000 601511679F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913171 5',
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                                                                                                                                                                                                       NIH-WGC http://wgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Londact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ArCC.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://wagge.llnl.gov

Plate: LLAM9732 row: n column: 20

High quality sequence stop: 387.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 GGACGTCCGGAGCGGGGGAGCAGTCCCCTCTCCATCAGGGAGTGGTCTATCTGGGCAGT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 CTGGGACCCAGGCACCGCGCCATCCCTGAGAGAGCAGCAGCAGCAGCAGCAGCATCTCA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NIH_MGC_71"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
106 c 46 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 387)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.6%; Score 355.8; DB 12;
llarity 98.7%; Pred. No. 6.5e-61;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3913171"
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                                                               mRNA sequence.
BE888168
BE888168.1 GI:10344201
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380; Conserv
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Best Local S
Matches 380
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ORIGIN
                                              DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
RESULT 8
BE888168
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(A)+ RNA was deposition of the possibility of the RNA was depositioned with bacterial alkaline pubsibilities (RAP) and then decapped with tabacco acid pyrophosphatase (RAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR I site by treatment of T4 RNA linker including ECOR I site by treatment of T4 RNA ligase and the first strand CDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The CDNA vector was circularized with E coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama Berg method. The obtained CDNA vectors were used for transformation of competent cells E. coli TOPIOF, by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kim, N.S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. R., Kim, N.S., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

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BM844470 425 bp mRNA linear EST 06-MAR-2002 K-EST0122585 S13KMS5 Homo sapiens cDNA clone S13KMS5-36-C10 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 425)
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Pred. No. 1.6e-60;
0; Mismatches 12
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/tissue_type="myeloma"
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/lab_host="Topl0F"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: yongsung@mail.kribb.re.kr
Plate: 36 row: C column: 10
High quality sequence stop: 425.
Location/Qualifiers
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DEFINITION
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VERSION
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
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Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                  Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
Obstaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.linl.gov
Seq primer: -40RP from Gibco
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Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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/db_xref="taxon:9606"
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Tel: 617-495-1812
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Site_10gan: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using Site_2: Sal 1; Starting library constructed using superscript plasmid Library kit (Life Technologies). CDNA made by oligo-dr priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library
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Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylle,T., Martin,J., Bliter,D., Walle,T., Marra,M., Pape,D., Wylle,T., Martin,J., Bennett,J.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas, M., Globons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Onpublished (2000)
Other_ESTS: 1648910.x1
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
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RPCI11-62K10.TJ RPCI-11 Homo saplens genomic clone RPCI-11-62K10,
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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Unpublished (1998)
Contact: Mark Adams
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Pred. No. 1.2e-52; .
0; Mismatches 116; Indels 0;
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0200
Fax: 301 838 0206
Email: mdadams@tigr.org
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BI793031 461 bp mRNA linear EST 12-MAR-2002 1647a04.yl Melton Normalized Human Islet 4 N4-HIS 1 Homo saplens CDNA clone IMAGE:5670030 5' similar to TR:075973 075973 CIQ-RELATED
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwoll, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylle, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Ohpublished (2000)
Other_ESTS: ie47a04.x1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pleter de Jong (pleter@deJong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html class: BAC ends.
                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/db_xref="GDB:7523673"
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/coll_ype="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC 16; Site_1 = 87 g 84 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1665 GGTCGTGGCTTCTCTTTTGTACAGAGGAGCGGGGGGGGTTTTAATAGCGGGCTCAGAGG
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1421 CGCTCGCCCTTCTCCCCG 1440
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                                                                                                                                              Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (brownefas.harvard.edu) This sequence now available from the IMAGE consortium, for clone orders contact: info@image.llnl.gov seq primer: 40RP from Gibco High quality sequence stop: 429.
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Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
AA 02138
Tel: 617-495-1812
Fax: 617-495-8557
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                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/clone="IMAGE:5670030"
/clone="IMAGE:5670030"
/sex="Both"
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Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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/dev_stage="Adult"
/lab_host="DH10B"
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Pred. No. 1.5e-51;
0; Mismatches 82;
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                                                                                                                                Email: dmelton@biohp.harvard.edu
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larity 81.4%;
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Email: dmetton@blohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 451.
Location/Qualifiers
1.540
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:5677849"
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BM354017 540 bp mRNA linear EST 12-MAR-2002 if29d01.yl Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:5677849 5' similar to TR:075973 075973 CIQ-RELATED
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by hydroxyapatite chromatography and used to make this
library."
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hiller, L., Marra, M., Pape, D., Wyller, T., Marra, M., Pape, D., Wylle, T., Martin, J., Blistain, A., Gibbons, M., McCann, R., Cole, R., Ronko, I., Bennett, J., Cardenas, Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium
Onpublished (2000)
Other_ESTs: 1f29d01.x1
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Harvard University, Howard Hughes Medical Institute
Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/dev_stage="Adult"
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                                                                                                        FACTOR.;, mRNA sequence.
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BM354017.1 GI:18086684
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76.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 617-495-8557
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Search completed: June 6, 2003, 20:53:01 Job time : 2940 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 2, 2003, 16:36:13 ; Search time 72 Seconds Run on:

(without alignments)
440.467 Million cell updates/sec

US-10-005-499-378 1311 1 WVLLLLVAIPLLVHSSRGPA......VHGGNINKYSTFSGFIIYPD 238 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

908470 segs, 133250620 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/SIDSZ/gcgdata/geneseq/genesegp-emb1/AA1994_DAT:
/SIDSZ/gcgdata/geneseq/genesegp-emb1/AA1995_DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Novel human secret	Novel human secret	Murine HSP47 inter	Human polypeptide	Novel human secret	Human CRF-like pro	Human polypeptide	Human polypeptide	Human polypeptide	Human polypeptide
ΩΙ	AAU84377	AAU84378	AAG64212	ABB53290	AAU09865	AAU76873	AAM39127	AAM40913	AAM38821	AAM40607
DB	23	23	22	23	23	23	22	22	22	22
% Query Match Length DB	238	267	255	255	287	225	744	755	253	255
% Query Match	100.0	98.1	69.2	68.89	66.3	50.5	28.7	28.7	26.8	26.8
Score	1311	1286.5	907.5	903.5	869.5	662.5	376	376	352	352
Result No.		7	m	4	ហ	9	7	80	6	10

A C X C X C X C X X X X X X X X X X X X

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(SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. (GLAX ) GLAXO GROUP LTD.
                                                      12-JUL-2000; 2000US-218033P. 21-AUG-2000; 2000US-226517P.
                           12-JUL-2001; 2001WO-US21985
17-JAN-2002.
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                                                                                                                                                                    The present invention relates to the isolation of novel human secreted or membrane-associated proteins and the genes encoding them. The sequences of the invention are useful for treating, preventing and ameliorating various diseases such as inflammatory disorders (e.g. ameliorating various diseases such as inflammatory disorders (e.g. asthma), neurological disorders (e.g. dementia), haematopoietic disorders, skeletal developmental disorders, growth abnormalities, neurodegenerative disorders (e.g. Huntington's disease), nervous system disorders, autoimmune disorders (e.g. Huntington's disease), nervous system clopheral myelinopathies, viral and bacterial infections, peripheral myelinopathies, viral and bacterial infections, hyper- and hypotension, obesity, bulimia, anorexia, manic depression, delirium, mental retardation, Tourette's syndrome, schizophrenia, growth, mental or sexual development disorders, and dysfunctions of the blood cascade the novel human secreted or membrane-associated proteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammatory disorder; neurological disorder; haematopoietic disorder; skeletal developmental disorder; growth abnormality; autoimmune disorder; neurodegenerative disorder; nervous system disorder; becterial infection; peripheral myelinopathy; viral infection; cancer; obesity; diabetes; hypotension; sexual development disorder; blood disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRRGKAGLRGPPGPPGPPGEPGRPGPPGPPGPGPGGVAPAAGYVPRIAFYAGLRRPH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                      Novel secreted and membrane-associated polypeptides and polynucleotides encoding the polypeptides, for preventing, treating and ameliorating cancers, mental or sexual developmental disorders, and malignant tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKYSTFSGFIIYPD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MVLLLLVAIPLLVHSSRGPAHYEMLGRCRMVCDPHGPRGPGPDGAPASVPFFPGAKGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVLLLLVAIPLLVHSSRGPAHYEMLGRCRMVCDPHGPRGPGPDGAPASVPPFPPGAKGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 100.0%; Score 1311; DB 23; Length 238; Local Similarity 100.0%; Pred. No. 8.3e-101; Los 238; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human secreted or membrane-associated protein #17
                                                                                                                                             Claim 1; Page 139-140; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU84378 standard; Protein; 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
   Xie
 Xiang Z,
                            WPI; 2002-188468/24
N-PSDB; ABK35597.
                                                                                                                                                                                                                                                                                                                                                                                                                       238 AA;
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 Smith RF,
                                                                                                                                                                                                                                                                                                                                                                                              Invention
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                                                                                                                                                                           Novel secreted and membrane-associated polypeptides and polynucleotides encoding the polypeptides, for preventing, treating and ameliorating cancers, mental or sexual developmental disorders, and malignant tumours
                                                                                                                                                                                                                                                                                                                                                                                                   or membrane-associated proteins and the genes encoding them. The sequences of the invention are useful for treating, preventing and ameliorating various diseases such as inflammatory disorders (e.g. asthma), neurological disorders (e.g. dementia), haematopoietic disorders, skeletal developmental disorders, growth abnormalities, neurodegenerative disorders (e.g. Huntington's disease), nervous system disorders, autoimmune disorders (e.g. theumatoid arthritis), neurologis, diabetes; cencers, malignant tumours, hypoteral myelinopathies, varial and bacterial infections, alpha-mannosidosis, diabetes, cancers, malignant tumours, hypotension, obesity, bulimia, anorexia, manic depression, delirium, mental retardation, Tourette's syndrome, schizophrenta, growth, mental or sexual development disorders, and dysfunctions of the blood cascade system including those leading to stroke. ANU84362-AAU84389 represent the novel human secreted or membrane-associated proteins of the
                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to the isolation of novel human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MYLLLLVAIPLLVHSSRGPAHYEMLGRCRMVCDPHGPRGPGPDGAPASVPPFPPGAKGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GRRGKA-------GLRGPPGPPGPRGPPGFPGPPG
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      Strum JC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.1%; Score 1286.5; DB 23; Length 267;
89.1%; Pred. No. 1e-98;
1ive 0; Mismatches 0; Indels 29;
   Lai Y, Martensen SA, Rizvi SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKLDGGKVHGGNTNKYSTFSGFIIYPD 238
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                                                                                                                                                                                                                                                                                                                        Claim 1; Page 140; 151pp; English.
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Cogswell JP, L.
Xiang Z, Xie Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 89.1
Matches 238; Conservative
                                                                                       WPI; 2002-188468/24.
N-PSDB; ABK35598.
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                                    Smith RF,
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AAG64212:
ID AAG6
XX
AC AAG6
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F4G64217

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placental disease; testicular cancer; male fertility; pancreatic disease.
                  antiinflammatory; antilipaemic; hepitotropic; virucide; antidiabetic; nephrotropic; anorectic; cytostatic; vaccine; neurological disease; cardiovascular disease; respiratory disease; liver disease; respiratory disease; liver disease; repetratory unscle disease; skeletal muscle disease; gastrointestinal disease;
neuroleptic; tranquiliser; antiarrhythmic; cardiant; antiasthmatic;
                                                                                                                                                                                                                                                                            6-APR-2001; 2001WO-US13360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-041392/05.
N-PSDB; ABA90355.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               asthma, amnesias
                                                                                                                                                                                             WO200181363-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xie Q;
                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                        01-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Lai Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 Y--VPRIAFYAGLRRPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGDGTSMWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGN 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 GAKGEVGRRGKAGLRGP---PGPPGPRGPP---GEPGR----PGPPGPPGPPGPGGVAPAAG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a method for preparing a protein which interacts with the heat shock protein HSP47. The method involves the two-hybrid screening method using the HSP47 gene and a mammalian CDNA library. The present sequence is the protein sequence for a murine HSP47 interacting protein, which was used in the present method. The HSP47 interacting proteins are useful for the diagnosis and treatment of diseases caused by an increase or decrease in activity of HSP47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVLLLLVAIPLLVHSSRGPAHYEMLGRCRMVCDPH-GPRGPG----PD-GAPASVPFFPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Using the two-hybrid screening method to prepare proteins which interact with the heat shock protein HSP47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine; heat shock protein interacting protein; HSP47.
                                                                                                                                                                                                                                                                                                                                                                 (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB53290 standard; Protein; 255 AA
                                                          Murine HSP47 interacting protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 23; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 NNKYSTFSGFIIYAD 255
                                                                                                                                                                                                                                                                              99JP-0330631
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                    (first entry)
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Best Local Similarity 70.23
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 TNKYSTFSGFIIYPD
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                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-395263/42.
N-PSDB; AAH48068.
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                                                                                                                                                                                        JP2001145493-A.
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                    19-SEP-2001
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55 GAKGEVGRRGKAGLRGP---PGPPGPRGPP---GEPGR---PGPPGPPGPGGVAPAAG 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       including congestive heart failure, flodgin's disease and myocardial infarction; respiratory diseases including asthma, chronic obstructive pulmonary diseases, cystic fibrosis and adult respiratory distances syndrome; liver diseases including hypercholesterolaemia, cirrhosis, syndrome; liver diseases including hypercholesterolaemia, cirrhosis, quocose tolerance; renal disease including renal failure, acute tubular necrosis and glomerulomephritis; skeletal muscle diseases including Eulenburg's disease, hypoglycaemia and obesity; gastrointestinal diseases including myofonia congenita and intestinal obstruction; lymph diseases including diseases of placenta including choriocarcinoma; diseases of testes including testicular cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated polypeptide comprising a 277, 480 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026, 844, 782, 262, 394, 411, 485, 286, 333, 495, 350, 619, 490, 462, 255, 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as given in the specification. The polypeptides, modulators of the polypeptides and antibodies against the polypeptides are useful for treating diseases such as neurological and psychiatric diseases including Alzheimer's, parasupranuclear palsy, Huntington's disease, myotonic dystrophy, anorexia and depression; cardiovascular diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MVLLLLVAIPLLVHSSRGPAHYEMLGRCRMVCDPH-GPRGPG----PD-GAPASVPPFPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 male reproductive diseases including low testosterone and male infertility; and disease of pancreas including diabetic Ketoacidosis, Type 1 and 2 diabetes and obesity. The present sequence is a Polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                   Kabnick KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polypeptides and polynucleotides useful as a vaccine for preventing and treating diseases associated the polypeptide, e.g. Alzheimer's disease, dyslipidemia, obesity, diabetes, infertility,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
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                                                                                                                                                                                                                                                                                                                                                   Smith RF, Xiang 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 101; 116pp; English.
                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP.
27-APR-2000; 2000US-199963P.
11-MAY-2000; 2000US-203336P.
25-MAY-2000; 2000US-207087P.
26-MAY-2000; 2000US-207546P.
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287 AA;

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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                    vaccines for inducing immunolists response in a mammal, and in screening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. The polypeptides can be used as immunogens to produce antibodies immunospecific for the polypeptides, and to identify membrane-bound or soluble receptors. The polypeptides, may be used as diagnostic reagents, in chromosome localisation studies and in tissue expression studies. The present sequence represents the amino acid sequence of novel human secreted protein #6.
                                                                                        GPKGEAGRPGKAGPRGPPGEPGPPGPMGPPGEKGEPGRQGLPGPPGAPGLNAAGAISAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New secreted proteins or polypeptides, useful for treating e.g. cancer, autoimmune diseases, wound healing disorder, infections, haematopoietic disorders, inflammatory disorders, infertility, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated novel secreted polypeptide (I) and polynucleotide (II). (I) and (II) are useful for treating cancer, autoimmune diseases, wound healing disorder, infections, haematopoietic disorders, inflammatory disorders, infertility, neurological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t
                                     YV - - PRIAFYAGLRRPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMR
                                                                           GGDGTSMWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGN
                                                                                                                                                                                                                                                                                                                                  antlinflammatory; neuroprotective; nephrotropic; cardiovascular; human; cancer; autolmmune disease; wound healing disorder; infection; haematopoietic disorder; inflammatory disorder; infertility; neurological disease; psychiatric disease; cardiovascular disease; respiratory disease; renal; gastrointestinal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        psychiatric diseases, cardiovascular diseases, respiratory diseases, renal diseases, or gastrointestinal diseases. These may also be used treat diseases, abnormalities and disorders caused by abnormal expression, production, function and/or metabolism of the genes, as
                                                                                                                                                                                                                                                                                                                         Secreted protein; cytostatic; immunosuppressive; vulnerary; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rizvi SK,
                                                                                                                                                                                                                     AAU09865 standard; Protein; 287 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 63-64; 92pp; English
                                                                                                                                                                                                                                                                                                Novel human secreted protein #6.
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BEECHAM PLC.
                                                                                                                             TNKYSTFSGFIIYPD 238
                                                                                                                                           2000US-196603P.
2000US-199417P.
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                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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24-APR-2000;
                                                                                                                                                                                                                                                                     26-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VINVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAIAQDADQ 191
                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                            1 MVLLLLVAIPLLVHSS-RGPAHYEMLGRCRMVCDPH------GPRG-----PGPDGAPAS 48
                                                                                                                                                                                                                                                                                                                         --PGPGGVAPAAGYV------PRIAFYAGLRRPHEGYEVLRFDDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V------PPFPPGAKGEVGRRGKAGLRGP---PGPPGPRGPPGEPGRPGPPGPPG--
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                                                                                                                                                 49; Gaps
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                                       Length 287;
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                                            DB 23;
                                                                                                                                                       44;
                                       Score 869.5; DB 2
Pred. No. 3.6e-64;
66.3%; Scores 59.6%; Pred. No. ...
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                                                                                               Local Similarity 59.69 to the searth of the search of the 
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                                                                                                                                                 Matches 171;
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                                                                                                                                                                                                                                      -----PGPGGVAPAAGY-------VPRIAFYAGLRRPHEGYEVLRFDD 130
                                                                                                                                                                                                131 VVINVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAIAQDAD 190
       and unipolar affective disorders, schizophrenia, olivopontocerebellar atrophy or Shy-Drager syndrome. The nucleotide sequences (or their complements) have various applications in the art of molecular biology, including uses as hybridisation probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. This sequence represents the human LP231 polypeptide of the invention.
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                                                                                                                                                               57
 synapse function, e.g. Parkinson's disease, Alzheimer's disease, bipolar
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J;
                                                                                                                         43;
                                                                                                     DB 23; Length 225;
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                                                                                                                                                                                                                                                                              Indels
                                                                                                                                           48 SVPPFPPGAKGEVGRRGKAGLRGPPGPPGPPGFPGFPGPPGPPGPPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oian XB,
Yang Y,
                                                                                                   50.5%; Score 662.5; DB 23;
57.0%; Pred. No. 3.7e-47;
11ve 17; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C, Asundi V, Chen R, Ma Y,
Ang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                          AAM39127 standard; Protein; 744 AA
                                                                                                                                                                                                                                                                                                                                                                                                        Human polypeptide SEQ ID NO 2272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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2000US-0598042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0620312
                                                                                                   Query Match
Best Local Similarity 57.0%
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-442253/47.
N-PSDB; AAI58283.
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Zhou P,
                                                                                225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-2000;
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09-JUL-2000;
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03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eukaemia.
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Wang J, 1
Zhao QA,
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                                                                                Sequence
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       he sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                625 PFPPVGAPVKENKLLYNGRQNYNDQTGIFTCEVPGVYFAYHVHCKGG---NVWVALFKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 PG-PGPGGV-----APAAGYVPRIAF-YAGLRRPH-------EGYEV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKY --STFSGFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 PHGPRG-PGPDGAPASVPPFPPGAKGEVGRRGKAGLRGPPGPPGPRGPPGEPGRPGPPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 744;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.7%; Score 376; DB 22; 37.2%; Pred. No. 7.2e-23; ive 31; Mismatches 77;
                                                                                               Example 4; SEQ ID NO 2272; 10078pp; English.
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Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          744 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 YP 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                             Human polypeptide SEQ ID NO 1966.
                        (first entry)
                                                                                                                                                                              WO200153312-A1
                                                                                                                                                                                                                                                                                                03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                         09-JUL-2000;
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                        22-OCT-2001
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Wang J, '
                                                                                                                                  enkaemia
 AAM38821;
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                                                                                                                                                                                                                                                                                             The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in game therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system autopathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the Activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 GQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKY--STFSGFII 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   636 PFPPVGAPVKFNKLLYNGRQNYNPQTGIFTCEVPGVYYFAYHVHCKGG---NVWVALFKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PG-PGPGGV-----APAAGYVPRIAF-YAGLRRPH-------EGYEV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                        Ren F, War Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77; Indels
                                                                                                                                                       Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.7%; Score 376; DB 22; 37.2%; Pred. No. 7.3e-23;
                                                                                                                                                   Liu C, Asundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ, Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                         Example 2; SEQ ID NO 5844; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Mismatches
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                                                                    2000US-0653450.
2000US-0662191.
2000US-0693036.
26-DEC-2000; 2000WO-US34263
                                                         2000US-0620312
                                                                                                         2000US-0727344
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Matches 90; Conservative
                                                                                                                                                                                                     WPI; 2001-442253/47
                                                                                                                                                                             Zhou P,
                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    755 AA;
                                                                                                                                                                                                                 N-PSDB; AAI60069
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                                                         19-JUL-2000;
03-AUG-2000;
                                                                                14-SEP-2000;
                                                                                                        29-NOV-2000;
                      21-JAN-2000;
                                   25-APR-2000;
                                               09-JUL-2000;
                                                                                              19-OCT-2000;
                                                                                                                                                                   Wang J, W
Zhao QA,
                                                                                                                                                       Tang YT,
Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous allocalised neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                 Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VLLLLVAIPLLVHSSRGPAHYEMLGRCRMVCDPHGPRGPGPDGAPASVPPFPPGAK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                 Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.8%; Score 352; DB 22; Length 253; 35.9%; Pred. No. 2.1e-21; ive 34; Mismatches 90; Indels 4
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                 Ma Y,
Xue AJ,
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Drmanac RT;
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                                                                                                                                                 2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
26-DEC-2000; 2000WO-US34263
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Les 93; Conservative
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N-PSDB; AAI57977.
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                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
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64 LPGLAGDHGEFGEKGDPGIPGNPGKVGPKGPMGPKGGPGAPGAPGPKGESGDYKA---TQ 120
                     RIAFYA-----GLRRPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLM 162
                                163 RGGDGTSMWADLMKNGQVRASAIAQDADQNYD---YASNSVILHLDVGDEVFIKLDGGKV 219
                                                                          ä
                                                                                                                                                                                                                                                                       cancer;
                                                                                                                                                                                                                                                                               peripheral nervous system; neuropathy; central nervous system; CNS; Alzhehmer is, Parkinson's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; chemotactic; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                      nootropic; immunosuppressant; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ren F,
Zhang J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   u C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; SEQ ID NO 5538; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen R,
Xu C,
                                                                                                                                                                                   Æ
                                                                                                                                                                                                                                                Human polypeptide SEQ ID NO 5538.
                                                                                                                      232 LLGMEGANSIFSGFLLFPD 250
                                                                                                       220 HGGNTNKYSTFSGFIIYPD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Asundi V, Che
Wehrman T, Xu
Goodrich R,
                                                                                                                                                                                 AAM40607 standard; Protein; 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
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2000US-0552317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                            26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                           (first entry)
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N-PSDB; AAIS9763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                  WO200153312-A1
                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2000;
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                                                                            177 RG-
                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                            35-APR-2000;
                                                                                                                                                                                                                           22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-2001
                                                                                                                                                                                                                                                                                                                           leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YT,
                                                                                                                                                                                                      AAM4 0607;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example
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                                                                                                                                                            RESULT 10
AAM40607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 RIAFYA-----GLRRPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLM 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides human breast specific coding sequences and proteins. These are useful for detecting breast tissue and for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     breast specific gene; breast cancer; gene therapy; breast disease;
                                                                                                                                                                                                                                                                                                                                                            65
Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                57
                                                                                            The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel breast-specific polypeptides and polynucleotides encoding polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating breast cancer and non-cancerous disease states in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 VLMLLLLLGLIDISQ---AQLSCTGPPAIPGIPGIPGTPGPDGQPG7----PGIKGEKG
                                                                                                                                                                                                                                                                                                                                                                                                              -----GEVGRRGKAGLRGPPGPPGPPGEPGEPGRPGPPGP-GPGGVAPAAGYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 RGGDGTSMWADLMKNGQVRASAIAQDADQNYD---YASNSVILHLDVGDEVFIKLDGGKV
                                                                                                                                                                                                                                                                                                                2 VLLLLVAIPLLVHSSRGPAHYEMLGRCRMVCDPHGPRGPGPDGAPASVPPFPPGAK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 LPGLAGDHGEFGEKGDPGIPGNPGKVGPKGPMGPKGGPGAPGAPGPKGESGDYKA---TQ
                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                42;
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                                                                                                                                                                                                            Length 255;
                                                                                                                                                                                                                                                                90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sun, Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cafferkey R,
                                                                                                                                                                                                              Score 352; DB 22;
Pred. No. 2.1e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human breast specific protein SEQ ID NO: 108
                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 225-227; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recipon H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 LLGMEGANSIFSGFLLFPD 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 HGGNTNKYSTFSGFIIYPD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABJ01025 standard; Protein; 638
                                                                                                                                                                                                                                                                34;
                                                                                                                                                                                                              26.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                   93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macina RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DIAD-) DIADEXUS INC.
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                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                    255 AA;
                                                                     C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO200240672-A2
                                                                                                                     specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-NOV-2000;
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                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                              28
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635 AA;
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20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
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                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                   72
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                                                                                                                                                                                                      Query Match
           Claim
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                                                                                                                                             AYHVLMRGGDGTSMWADLMKNGQVRASAIAQDADQNY-DYASNSVILHLDVGDEVFIKLD 215
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AYHUHVK---GINVWVALYKN-NVPATYTYDEYKKGYLDQASGGAVLQLRPNDQVWVQMP 613
                                                                                           74
                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu C, Cao Y, Ma Y;
R, Wang ZW;
                                                                                                             394 RGPSGIPGL------QGPAGPIGPQGLPGLKGEPGLPGPPGE-GRAGEPGTAGPTGP
                                                                                                                                 75 PGPRGPPGEPGRPGPPGPPGPGPGCVAPAAGYVPRIAFYAGLRRPHEGYE-----
                                                                                                                                                                                    ::|| : | |:| ||||: |||:|
498 QFGLGELSAHATPAFTAVLTSPFPASGMPVKFDRTLYNGHSGYNPATGIFTCPVGGVXYF
                                                                                           RGPAHYEMLGRCRMVCDPHGPRGP-GPDGAPA-SVPPFPPGAKGEVGRRGKAGLRGPPGP
                                                                                                                                                                       ------BARGKETCPMPGVYFF
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
and treating breast cancer and other breast diseases. The present sequence is a breast specific polypeptide of the invention.
                                                                     63;
                                                  DB 23; Length 638;
                                                ; Score 345.5; DB 23; Length
; Pred. No. 2e-20;
30; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asundi V, Zhou P,
ing J, Ren F, Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                       nervous system disorder; arthritis; inflammation.
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Wang J, Zhang J, Ren
Wejhrman T, Goodrich R;
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614 SDQANGLXSTEYIHSSFSGFLLCP 637
                                                                                                                                                                                                                                                      216 GGKVHGGNTNKY -- STFSGFIIYP 237
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                                                                                                                                                                                                                                                                                                                          AAM78798 standard; Protein; 635
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2000US-0663561.
2000US-0693325.
                                                                                                                                                                                                                                                                                                                                                                                       Human protein SEQ ID NO 1460.
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2000US-0560875.
2000US-0598075.
                                                ch 26.4%;
1 Similarity 35.6%;
94; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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N-PSDB; AAK51931.
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Wang D,
Yang Y, W
                                                           Local Similarity
                             638 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157190-A2
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15-SEP-2000;
20-OCT-2000;
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Zhao QA,
                                                                                                                                                                        125
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                              Sequence
                                                  Query Match
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                                                                                                                                                                                                                                                                                                       RESULT 12
AAM78798
                                                                     Matches
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/lnhibin activity and may be useful in the diagnosis and/or inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------PGPP-----GPRGPPGEPGRPGPPG-PGPGGVAPAAGYV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               471 TGI---AGLHLPNGGVEGAVLGKGGKPQFGLGELSAHATPAFTAVLTSPLPASGMPVKFD 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 DVVINVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAIAQDA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          528 RILYNGHSGYNPATGIFTCPVGGVYYFAXHVHVK---GINVWVALKKN-NVPATYTYDEY 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 HGPRGP-GPDGAPA-SVPPFPPGA-----KGEVGRRGKAGLRGP------71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemla; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                 Note: Note: SECOID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 DQNY-DYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKY--STFSGFIIYP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 635;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.3%; Score 345; DB 22;
33.0%; Pred. No. 2.2e-20;
iive 32; Mismatches 67;
20; Page 3730-3731; 6221pp; English.
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2000US-0598075.
2000US-0620325.
2000US-0654936.
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us-10-005-499-378.rag

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13;
                                                                                                                                                                                                                                                                                              The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAIAQDA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          592
                                                                                                                                                                                                                                                                                                                                           production of other cytokines in other cell populations. The population of other cytokines in other cell populations. The polymerlectides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity infinibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
                                                                                                       Υ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480 TGI---AGLHLPNGGVEGAVLGKGGKPQFGLGELSAHATPAFTAVLTSPLPASGMPVKFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      537 RILYNGHSGYNPATGIFTCPVGGYYYFAYHVHVK---GTNVWVALYKN-NVPATYTYDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                        Ma
                                                                                                                                                                                                                Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
                                                                                                  LC, Cac
Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DQNY-DYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKY--STFSGFIIYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.3%; Score 345; DB 22; Length 644; 33.0%; Pred. No. 2.3e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 HGPRGP-GPDGAPA-SVPPFPPGA-----KGEVGRRGKAGLRGP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                     Xu
R,
                                                                                                  Asundi V, Zhou P,
ang J, Ren F, Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ovarian antigen HDHEB13, SEQ ID NO:2619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32; Mismatches
                                                                                                   Liu C, Drmanac RT, Asundi V,
Wang D, Wang J, Zhang J, Ren
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                               Claim 20; Page 332; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP41487 standard; Protein; 314 AA
15-SEP-2000; 2000US-0663561.
20-OCT-2000; 2000US-0693325.
30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                      Liu C, Li
                                                                                                                                                                WPI; 2001-476283/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            644 AA;
                                                                  (HYSE-) HYSEQ INC
                                                                                                                                                                                     N-PSDB; AAK52915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-AUG-2002
                                                                                                  Tang YT,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                     Kue AJ,
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The invention transes to 217 hover indian ovarian unitagens (ABP41228) and to cobhas encoding them (ABD64131-ABD65635), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the theoriton. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides against human ovarian antigens and the use of ovarian antigens prognosing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and metastratic tunnours of ovarian or breast origin, reproductive system of isorders (e.g., infertinity, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infertinity, disorders of pregnancy, anovulation.

CC shock syndrome, inflammatory conditions (e.g., mastitis, cophoritis and varianties), immune disorders (e.g., congenital and acquired thematory conditions (e.g., mastitis, sophoritis and toward inflammatory conditions (e.g., mastitis, sophoritis and unitary system disorders (e.g., congenital and acquired thematory disorders (e.g., anamia), cardiovascular disorders.

CC shock syndrome), inflammatory conditions (e.g., mastitis, system), conditions (e.g., anamia), cardiovascular disorders.

CS shock system disorders (e.g., anamia), cardiovascular disorders.

CC and unianzy system disorders. Ovarian antigen polypeptides and conditions of the polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may also be used in screening for compounds which contentification of individuals and in forensic analysis, and the content esquence acts for gene therapy, chromosome mapping, in the citetine of individuals and in forensic analysis, and the printed sequence represents a human ovarian antigen of the invention.

CC sequence represents a human ovarian antigen of the invention.

CC sequence represents a human ovarian antigen of the invention at the va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory condition; immune disorder; blood disorder;
cardiovascular disorder; respiratory disorder; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to 2175 novel human ovarian antigens (ABP41054-
                                                                     gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.1%; Score 329.5; DB 23; Length 314; 33.6%; Pred. No. 2e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 GRCRMVCDPHGPRG-PGPDGAPA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; SEQ ID No 2619; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-2000; 2000US-209467P.
                                                                                                                                                                                                                                                                                                                                             07-JUN-2001; 2001WO-US18569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-147878/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABQ54564
                                                                                                                                                                                                                                              WO200200677-A1.
                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                               03-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                         RIAFYAGLRR--PHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGD 166
                                                                                             167 GTSMWADLMKNGQVRASAIAQDADQ-NYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTN 225
Mus musculus ACRP3ORIM useful for identifying agonist and antagonist of
the protein, which is useful for treating and preventing diseases such
as cancers, inflammation, cell death, obesity, diabetes, heart disease
                                                        Murine; gene therapy; cytostatic; antiinflammatory; antiidiabetic; cardiant; anorectic; ACRP3OR1M; cancer; inflammation; cell death; obssity; diabetes; heart disease; cell proliferation; immunity; energy metabolism; homeostasis; ACRP3O; Adipocyte Complement-Related Protein of 30 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 25.1%; Score 329; DB 21; 3 Similarity 32.7%; Pred. No. 1.9e-19; 86; Conservative 33; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 23-24; 28pp; English.
                                                                                                                                                                                                                                                 AAB37344 standard; Protein; 285 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhu Y;
                                                                                                                                                   KY---STFSGFIIYPD 238
                                                                                                                                                                  292 PYWTDSLFTGFLIYAD 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-2000; 2000WO-US11606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       990S-0131379.
20000S-0559439.
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith RF, Li X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-687315/67
N-PSDB; AAC67788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 AA;
                                                                                                                                                                                                                                                                                                                                   Murine ACRP30R1M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-APR-2000;
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                                        109
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26 GRCRMVCDPHGPRG-PGPDGAPASV-----

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Gaps

64;

Indels

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143 --CGSSRAKSAFSVAVTKSYPRERLPIKFDKILMNEGGHYNASSGKFVCSVPGIYYFTYD 200
                                                                        57 KGEVGRRGKAGLRGPPGPPGPPGPPGEPGRPGPPGPPGP----GPGGVAPAAGYVPRIA 111
                                                                                                                                                                         112 FYAGLRRPHEGYEV-----LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYH 159
                                                                                                                                                                                                                                                                            160 VLMRGGDGTSMWADLMKNGQVRASAIAQDADQ-NYDYASNSVILHLDVGDEVFIKLDGGK 218
                                                                                                                                                                                                                                                                                                      219 VHGGNTNKY---STFSGFIIYPD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: June 2, 2003, 16:45:31
Job time : 74 secs
                                                                                                                                                                                                                                                                                                                                                                                                                              256 QNGLFYDPYWTDSLFTGFLIYAD 278
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us-10-005-499-378.rsp

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 2, 2003, 16:36:54 ; Search time 21 Seconds (without alignments) 470.065 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-005-499-378 1311 1 MVLLLLVAIPLLVHSSRGPA......VHGGNTNKYSTFSGFIIYPD 238

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

																																		•
	Description	O88992 mus musculu	075973 homo sapien	O9esn4 mus musculu	Q00780 mus musculu	P14282 oryctolagus		P27658 homo sapien	homo	gallu	P23206 bos taurus	homo	homo	homo	homo	homo	mus π	Q9bxj2 homo sapien	mus m	P31721 rattus norv	P02745 homo sapien	P14106 mus musculu	P98086 mus musculu	Q9bxj0 homo sapien	Q9bxj4 homo sapien	P98085 lepomis mac	Q06576 tamias sibi	Q06577 tamias sibi	P98087 rattus norv	Q9bxi9 homo sapien	Q9r171 mus musculu	рошо	homo sa	Q06575. tamias sibi
SUMMARIES	ID	C1RF_MOUSE	C1RF_HUMAN	GLIC_MOUSE	CA18_MOUSE	CA18_RABIT	CA1A_MOUSE	CA18_HUMAN	CA1A_HUMAN	CA1A_CHICK	CAIA_BOVIN	C1QB_HUMAN	CA28_HUMAN	CQT2_HUMAN	C1QC_HUMAN	APM1_HUMAN	APM1_MOUSE	CQT7_HUMAN	C1QC_MOUSE	C1QB_RAT	C1QA_HUMAN	Clob_Mouse .	C1QA_MOUSE	CQT5_HUMAN	CQT3_HUMAN	COLE_LEPMA	HP25_TAMSI	HP27_TAMSI	CERL_RAT .	CQT6_HUMAN	CERB_MOUSE	CERL_HUMAN	CERB_HUMAN	HP20_TAMSI
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	Query Match Length DB	258	258	255	743	744	680	744	9	674	674	251	635	282	245	244	247	289	246	253	245	253	245	243	246	419	215	215	224	278	193	201	193	196
de	Query Match	70.0	6.69	69.5	30.3	29.6	28.7	28.7	27.7	27.5	27.5	26.8	26.3	25.0	24.9	24.3	24.2	24.1	24.1	24.1	24.0	23.1	23.0	22.9	21.9	21.8	20.5	19.9	18.5	18.2	17.6	17.6	17.5	17.0
	Score	918	917	907.5	397	388.5	376	376	362.5	360.5	360	352	345	328	327	318	317.5	316.5	316	316	314	302.5	302	300	287	285.5	268.5	261.5	243	239	231	230.5	229	222.5
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	PO2452 homo sapien Q9xs17 canis famil				
CQT1_HUMAN	CA11_HUMAN	CA39_CHICK CA44_BOVIN	CA13_HUMAN CA1H_MOUSE	CA12_MOUSE CA1H_HUMAN	CQT4_HUMAN CA11_BOVIN
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281	1464 1460	675 453	1466 1527	1459	329 779
16.5	16.1	16.0	15.9 15.8	15.8 15.8	15.7
216.5	211.5	209.5 208	208 207	206.5	206 205.5
ይ ራ 4 ሊ	36 37	38 39	40	43	44 45

ALIGNMENTS

SULT 1 RF_MOUSE CIRF_MOUSE STR 088992;			•		Query Match 70.0%; Score 918; DB 1; Length 258; Best Local Similarity 68.6%; Pred. No. 4.8e-53;
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POTENTIAL.

C10; 1.

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PROSITE; PS01113;
              Collagen; Signal.
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                                                                             SEQUENCE
                                                                                                      Query Match
Best Local
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                                                                                                                 121 TATYTVPRVAFYAGLKNPHEGYEVLKEDDVVTNLGNNYDAASGKFTCNIPGTYEFTYHV 180
                                                                                                                                                                  160
                                                  FPPGAKGEVGRRGKAGLRGPPGPPGPRGPP-----GEPGRPGPPGPPGPGPGVAP 102
                                                                                                                                                      161 LMRGGDGTSMWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVH 220
 51
MVLLLLVAIPLLVHSSRGPAHYEMLGRCRMVCDPHGPRGPG----PDGAPA----SVPP
|-|:|:|:|| ||:|| |
              103 AAGY--VPRIAFYAGLRRPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi
Nickerson D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

BELLINE-9097006; PubMed-987855;
Berube N.G., Swanson X.H., Bertram M.J., Kittle J.D., Didenko V., Baskin D.S., Smith J.R., Pereira-Smith O.M.;
Cloning and characterization of CRF, a novel Clq-related factor, expressed in areas of the brain involved in motor function.";
Brain Res. Mol. Brain Res. 63:233-240(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE.

TISSUE-Placenta;
Strausberg R.;
Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-!- TISSUE SPECIFICITY: EXPRESSED IN BRAINSTEM.
-!- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
-!- SIMILARITY: CONTAINS 1 C10 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF095154; AAC64186.1; -.
EMBL; AF410771; AAK95548.1; -.
EMBL; BC006798; AAH08798.1; -.
InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF01391; Collagen; 1.
Pfam; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1.
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16-0CT-2001 (Rel. 40, Last seque
15-JUN-2002 (Rel. 41, Last annot
Clg-related factor precursor.
ClQRF OR CRF.
Homo saplens (Human)
                                                                                                                                                                                                        221 GGNTNKYSTFSGFIIYPD 238
                                                                                                                                                                                                                       241 GGNSNKYSTFSGFIIYSD 258
                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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075973;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
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                                                                                                                                                                                                                          1 MVLLLLVAIPLLVHSSRGPAHYEMLGRCRMVCDPHGPRGPG----PDGAPA----SVPP
                                                                                                                                                                                                                                                 103 AAGY--VPRIAFYAGLRRPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHV
                                                                                                                                                                                                                                                                                                                                                                                                                              121 TATYTTVPRVAFYAGLKNPHEGYEVLKFDDVVTNLGNNYDAASGKFTCNIPGTYFFTYHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 LMRGGDGTSMWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20428709; PubMed=10862616;
MEDLINE-20428709; PubMed=10862616;
Koide T., Aso A., Yorihuzi T., Nagata K.;
"Conformational requirements of collagenous peptides for recognition
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                               20;
                                                                                                                                   Length 258;
                                                                                                                                                                               Indels
                                                                                       52C51CDF59CAE2BF CRC64;
                                                                                                                                                                                 43;
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                                                                                                                                69.9%; Score 917; DB 1;
69.8%; Pred. No. 5.5e-53;
ive 15; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alacolin precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 AA
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InterPro; IPR001073; CIq.
InterPro; IPR001073; CIq.
Pfam; PP01381; Collagen.
PRINTS; PR00007; COMPLEMNTCIQ.
SMART; SM00110; CIQ; 1.
PROSITE; PS01113; CIQ; 1.
Collagen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GGNSNKYSTFSGFIIYSD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 GGNTNKYSTFSGFIIYPD 238
                                                                                       26452 MW;
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                                                                                                                                                                          Matches 180; Conservative
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16
258
115
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67
123
258 AA;
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CONFLICT
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X REDLINE-21085660; PubMed-11217851;

A RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Evkunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Baralov S., Casavant T.,

R Actim I. L., Ashburner M., Baralov S., Casavant T.,

R Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

R Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schrim I. L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GGDGTSMWADLCKNNQVRASAIAQDADQNYDYASNSVVLHLEPGDEVYIKLDGGKAHGGN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                              55 GAKGEVGRRGKAGLRGP---PGPPGPRGPP---GEPGR---PGPPGPPGPGPGGVAPAAG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y--VPRIAFYAGLRRPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMR 163
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                              DB 1; Length 255;
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Muragaki Y., Shiota C., Inoue M., Ooshima A., Olsen B.R.,
                                                                                                                                                                                                                                                         Indels
                                                                                                                            529FBAF4B2191BC1 CRC64;
                                                                                                                                                                                        69.2%; Score 907.5; DB 1; 70.2%; Pred. No. 2.2e-52; ive 18; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA18_MOUSE STANDARD; PRT; 743 AA. 000780; 09D2V4; 01-NOV-1995 (Rel. 32, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Collagen alpha 1(VIII) chain precursor.
   POTENTIAL.
GLIACOLIN.
COLLAGEN-LIKE.
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2687 MW;
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241 NNKYSTFSGFIIYAD 255
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Matches 179; Conservative
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                                                                                                                                                                                                                                                                                                                                        -!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
-!- SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.
-!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                               HENDERLING MAJOR COMPONENT OF THE DESCEMET'S MEMBRANE (BASEMENT SEGURITY OF CORNEAL ENDOTHELIAL CELLS.
-!- SUBUNIT MAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN ASSOCIATION WITH ALPHA ZIVIII) TYPE COLLAGENS.
-!- TISSUE SPECIFICITY: HIGH LEVELS IN CALVARIUM, EYE & SKIN OF NEWBORN MICE; ALSO IN VARIOUS EPITHELIAL, ENDOTHELIAL AND
                                                                                  "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Connective tissue; Repeat; Hydroxylation; hesion; Collagen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOLLAGEN ALPHA 1 (VIII) CHAIN.

COLLAGEN ALPHA 1 (VIII) CHAIN.

COLLAGEN ALPHA 1 (VIII) CHAIN.

NONHELICAL REGION (NC2).

TRIPLE-HELICAL REGION (NC1).

G -> R (IN REF. 2).

H -> Y (IN REF. 1).

F -> L (IN REF. 1).

P -> A (IN REF. 1).

P -> A (IN REF. 1).

T -> SR (IN REF. 1).

T -> P (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F584D85BD53897F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, X66976; CAA47387.1; --
EMBL, X66977; CAA47387.1; JOINED.
EMBL, AKO18742; BAB31383.1; --
PIR; S23779; S23779.
MGD; MGI: 88463; CO1881.
InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00386; Clq; 1.
Pram; PF001391; Collagen; 7.
PRINTS; PR00007; COMPLENRTC1Q.
SMART; SM00110; ClQ; 1.
Extracellular matrix; Connective
Glycoprotein; Cell adhesion; Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73454 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94; Conservative.
                                                                                                                                                                                                                                                                                                                   MESENCHYMAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         743 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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172 ADLMKNGOVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKY--ST 229
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                                                                                                                 PGPPGPPG-PGPGGV----APAAGYVPRIAF-YAGLRRPH------EGYEV--- 125
                                                                                                                                                                                                                            ------LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMW 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93143676; PubMed-8424763;
Ellma K., Eerola I., Rosatl R., Metsaranta M., Garofalo S., Perala M.,
de Crombrugghe B., Vuorio E.;
"The mouse collagen X gene: complete nucleotide sequence, exon
structure and expression pattern.";
Blochem. J. 289:247-253(1993).
                                                                                                                                                                                                                                                                TAELTAPFPPVGAPIKFDRLLYNGRQNYNPQTGIFTCEVPGVYFAYHVHCKGG---NVW
                                                        502 ITGPSGPIGPPGIPGPKGEPGL--PGPPGFPG-VGKPGVAGLHGPPGKPGALGPQGQPGL
  31 VCDPHGPRG----PGPDGAPASVPPFPPGAKGEVGRRGKAGLRGPPGPPGPPGPPGFPGR
                                                                                                                                                                         PGPPGPPGPPGPPAVMPPTPAPQGEYLPDMGLGIDGVKTPHAYAAKKGKNGGPAYEMPAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Intron-exon structure, alternative use of promoter and expression of the mouse collagen X gene, Coll0a-1."; Eur. J. Biochem. 213:99-111(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes and mapping of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Elima K., Metsaeranta M., Kallio J., Peraelae M., Eerola I.,
Garofalo S., de Crombrugghe B., Vuorio E.;
"Specific hybridization probes for mouse alpha 2(IX) and alpha 1(X)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRLIN-129/SV: TISSUE-Liver;
STRLIN-129/SV: TISSUE-Liver;
MEDLINE-93238750; Pubmed-8477738;
KODG R.Y.C., Kwan K.M., Lau E.T., Thomas J.T., Boot-Handford R.P.,
Grant M.E., Cheah K.S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collagen mRMAS.";
Blochim. Blophys. Acta 1130:78-80(1992).
-!- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHONDROTOCYTES AND HAS BEEN LOCALIZED. TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apte S.S., Seldin M.F., Hayashi M., Olsen B.R.; "Cloning of the human and mouse type X collagen the mouse type X collagen gene to chromosome 10. Bur. J. Blochem. 206:217-224(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collagen alpha 1(X) chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92182017; PubMed-1543751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92267014; Pubmed-1587271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 385-627 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 51-680 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBUNIT: HOMOTRIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 FSGFIIYP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-DBA/2J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAIA_MOUSE
Q05306;
                                                                                                                 87
                                                                                                                                                                                                                                  126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89380199; PubMed-2476437;

MEDLINE-89380199; PubMed-2476437;

A maguchi N. Benya P.D., van der Rest M., Minomiya Y.;

"The cloning and sequencing of alpha 1(VIII) collagen conversate that type VIII collagen is a short chain collagen and carboxyl-terminal non-triple-helical

"The cloning tiple helical and carboxyl-terminal non-triple-helical

"The contains tiple helical and carboxyl-terminal non-triple-helical

"The standard connection of the description of the triple helical

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"The collagent of the triple helical and the present of the tribe helical region of the tribe helical second of the triple helical second o
Gaps
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Sukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01113; C10; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47;
                                                                                                                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Collagen alpha 1(VIII) chain precursor (Endothelial collagen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.6%; Score 388.5; DB 1; Length 744; 37.5%; Pred. No. 2.2e-18; Live 30; Mismatches 78; Indels 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLLAGEN ALPHA 1(VIII) CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2A8CEF1EF8274E99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell adhesion; Collagen; Signal.
                                                                                                                                                                                                                                                                                        744 AA.
                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00386; Ciq; 1.
Pfam; PF01391; Collagen; 8.
PRINTS; PR00007; COMPLEMNTC1Q.
SMART; SM00110; CiQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A34246; A34246.
InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73358 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J05042; AAA31204.1; -.
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                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                   231 SGFIIYP 237
                                                                                                                       SGYLLYP 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              744 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SIGNAL
                                                                                                                                                                                                                                                                                     CA18_RABIT
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Matches
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MIM; 120251;
                                                                                                                                                                                                                                                                                      TISSUE=Lung;
                                       CA18_HUMAN
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DOMAIN
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensee agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPHEGYEV-LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKY--STFSGFI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPRG----PGPDG--APASVPPFP-----PGAKGEVG--RRGKAGLRGPPGPPGPRG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Gaps
-1- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXICATED IN SOME OR ALL OF THE CHAINS.
-1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
-1- SIMILARITY: CONTAINS 1 C10 DOMAIN.
                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01113, C10, 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.7%; Score 376; DB 1; Length 680,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77; Indels
                                                                                                                                                                                                                                                                                                                                                                                             COLLAGEN ALPHA 1(X) CHAIN.
NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FE984CA99AF708E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 PPGEPGRPGPPGPGPGGVAP----AAGYVPRI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FD -> IY (IN REF. Q -> T (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.3e
31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; 522215; 52215.
MGD; MGI:88445; Coll0al.
InterPro; IPR0001073; Clq.
InterPro; PR000087; Collagen.
Pfam; PF00386; Clq, 1.
Pfam; PF01391; Collagen; 9.
                                                                                                                                                                                                                                                                                                      PRINTS: PRO0007; COMPLEMNTC1Q. ProDom; PD000007; Collagen; 2. SWART; SW00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66775 MW;
                                                                                                                                                                   X65121; CAA46237.1; -. X63013; CAA44741.1; -. Z21610; CAA79736.1; -.
                                                                                                                                                          EMBL; X67348; CAA47763.1; -.
                                                                                                                                                                                                                                                                                                                                                                      Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.48;
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                                                                                                                                                                                                                                                                                                                                                                   Cartilage; Collagen;
                                                                                                                                                                                                                       S31216; S31216.
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les 91; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE-91231001; PubMed-2029894;
Muragaki Y., Mattei M.-G., Yamaguchi N., Olsen B.R., Ninomiya Y.;
Muragaki Y., Mattei M.-G., Yamaguchi N., Olsen B.R., Ninomiya Y.;
"The complete primary structure of the human alpha 1 (VIII) chain and assignment of its qene (COLBA1) to chromosome 3.";
Eur. J. Blochem. 197:615-622(1991).
                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PSOILI3; ClQ; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Civenorotein; Cell adhesion; Collagen; Signal.
                P27658; Q96D07;
01-AUG-1992 (Rel. 23, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Collagen alpha 1(VIII) chain precursor (Endothelial collagen).
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NONHELICAL REGION (NC2).
TIPLE-HELICAL REGION (COL1).
NONHELICAL REGION (NC1).
744 AA.
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InterPro; IPR000087; Collagen.
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Pfam; PF01391; Collagen; 8.
PRINTS; PR000007; COMPLEMNTC1Q.
Probom; PD000007; Collagen; 1.
SWART; SM00110; ClQ; 1.
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PIR; S15435; S15435.
Genew; HGNC:2215; COL8A1.
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                                                                                            PGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHAYGAKKGKNGGPAYEMPAFTAELTA
                                                                                                                                                                       PFPPVGAPVKFNKLLYNGRQNYNPQTGIFTCEVPGVYYFAYHVHCKGG---NVWVALFKN
                                                                                                                        PG-PGPGGV-----BPAAGYVPRIAF-YAGLRRPH------EGYEV-----
                                                                                                                                                             -----LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKN
                                                                                   PHGPRG-PGPDGAPASVPPFPPGAKGEVGRRGKAGLRGPPGPPGPRGPPGRPGPPGP
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=91109659; Pubmed=1764025; Thomas J.T., Cresswell C.J., Rash B., Nicolai H., Jones T., Solomon E., Grant M.E., Boot-Handford R.P.; "The human collagen X gene. Complete primary translated sequence and chromosomal localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic organization and full-length cDNA sequence of human collagen
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93012005; PubMed-1397333; Reichenberger E., Beier F., Luvalle P., Olsen B.R., von der Mark K., Bertling W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes and mapping of
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                  44;
                                              Length 744;
                                                                  77; Indels
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Beier F., Lammi M.B., von der Mark K.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
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A -> H (IN REF. 1).
Y -> T (IN REF. 1).
A -> G (IN REF. 1).
; 2BC1B0955DE2C9A3 CRC64;
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                                               DB 1;
                                                        1.4e-17;
                                                                                                                                                                                                                                                                                              CAIA_HUMAN STANDARD; PRT; 680 AA. 003692; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) collagen alpha 1(X) chain precursor.
                                                                 31; Mismatches
                                               Score 376;
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                                                          Pred.
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                             73364 MW;
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                                               28.78;
37.28;
                                                                 Conservative
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464
601
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744 AA;
                                                        Similarity
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Best Local S.
Matches 90
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 547-655 FROM N.A.
MEDLINE-92077285; PubMed-1743401;
Relichenberger E., Adgrer T., von der Mark K., Stoeb H., Bertling W.;
In situ hybridization studies on the expression of type X collagen in fetal human cartliage.";
Dev. Biol. 148:562-572(1991).
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MEDIARE-9518149; PubMed-7876225;
Chan D., Cole W.G., Rogers J.G., Bateman J.F.;
"Type x collagen multimer assembly in vitro is prevented by a Gly618 to Val mutation in the alpha l (x) NCl domain resulting in Schmid metaphyseal chondrodysplasia.";
J. Biol. Chem. 270:4558-4562(1995).
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Wallis G.A., Rash B., Sweetman W.A., Thomas J.T., Super M., Evans Grant M.E., Boot-Handford R.P.;
"Amino acid substitutions of conserved residues in the carboxyl-terminal domain of the alpha 1(X) chain of type X collage occur in two unrelated families with metaphyseal chondrodysplassia type Schmid.";
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MEDLINE-94272470; PubMed-8004099;
MCINCOSh I., Abbott M.H., Warman M.L., Olsen B.R., Francomano C.
"Additional mutations of type X collagen confirm COLIOAl as the
Schmid metaphyseal chondrodysplasia locus.";
Hum. Mol. Genet. 3:303-307(1994).
                                                                                                                                                                                      DNA and localization of human chromosome 6.";
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                                                                   SEQUENCE OF 561-666 FROM N.A.
MEDLINE=91243838; PubMed=2037056;
Apte S., Mattei M.-G., Olsen B.R.;
"Cloning of human alpha 1(X) collagen
COLIOA1 gene to the q21-q22 region of
FEBS Lett. 282:393-396(1991).
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Eur. J. Biochem. 206:217-224(1992).
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-1- SIMILARITY: STRONG, TO ALPHA I AND 2 TYPE VIII COLLAGENS.
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Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Cartilage; Collagen; Signal; Disease mutation; Polymorphism. SIGNAL 1 POLYMORENTIAL.
                                                                              MEDLINE-99057503; PubMed-9837818;
Ikegawa S., Nishimura G., Nagai T., Hasegawa T., Ohashi
                                                                                                                                                                                         Mutation of the type X collagen gene 'COL10A1' causes
                                                                                                                                                                                                                                       spondylometaphyseal dysplasia.";
Am. J. Hum. Genet. 63:1659-1662(1998)
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InterPro; IPR000087; Collagen.
Pfam; PF01381; Clq; I.
Pfam; PF01391; Collagen; B.
PRINTS; PR00007; COMPLENNTC10.
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[15]
VARIANTS SMD GLU-595.
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EMBL, X72579; CAASILY
EMBL, X72580; CAASILY
PIR, S10865; S15826.
PIR, A43901; A43901.
PIR, S18249; S18249.
PIR, S26396; S26396.
                                                                                                                                                                                                                                                                                                                                                      VARIANT SMCD CYS-597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 120110; -.
MIM; 156500; -.
MIM; 184250; -.
                                                                                                                                                            Nakamura Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MBL;
TWENT BEAR AND BEAR A
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                                                                                                                                                                                                                                                                                             90 PGPPGPGPG------GVAPAAGYVPRIAFYAGLR-RPHEGYEV------ 125
                                                                                                                                                                                                                                                                                                                                                                                                   126 LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAI 185
                                                                                                                                                                                                                                                                                                                                                                                                                     510 PGPPGP-PGQAVMPEGFIKAGQRPSLSGTPLVSANQGVTGMPVSAFTVILSKAYPAIGTP
                                                                                                                                                                                                                                                                             34 PHGPRG----PGPDGAPASVPPFPPGAKGEVGRRGKAGLRGPPGPPGPPGEPGRPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-75 FROM N.A. MEDILINE=89054019; PubMed=2461368; MEDILINE=89054019; PubMed=2461368; Luvalle P., Ninomiya Y., Rosenblum N.D., Olsen B.R.; "The type X collagen gene. Intron sequences split the 5'-untranslated region and separate the coding regions for the non-collagenous aminoterminal and triple-helical domains."; Lerminal and triple-helical domains."; Biol. Chem. 263:18378-18385(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 AQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKY--STFSGFIIYP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              626 DEYTKGYLDQASGSAIIDLTENDQVWLQLPNAESNGLYSSEYVHSSFSGFLVAP 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The developmentally regulated type X collagen gene contains a long open reading frame without introns."; J. Blol. Chem. 261:5041-5050(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 48-674 FROM N.A., AND SEQUENCE OF 103-117 AND 453-466. MEDLINE-86168227; PubMed=3082876;
Ninomiya Y., Gordon M., van der Rest M., Schmid T., Linsenmayer T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS TO C-TERMINUS.
MEDLINE-89380199; PubMed=2476437;
Yamaquchi N., Benya P.D., van der Rest M., Ninomiya Y.;
Tamaquchi N., Benya P.D., van der Rest de Cloning and sequencing of alpha 1(VIII) collagen cDNAs demonstrate that type VIII collagen is a short chain collagen and contains triple-helical and carboxyl-terminal non-triple-helical domains similar to those of type X collagen.";
                                                                                                                                                                                                                                             37;
                                                                                                                                                                                                              Score 362.5; DB 1; Length 680;
Pred. No. 9.7e-17;
3; Mismatches 78; Indels 37
COLLAGEN ALPHA 1(X) CHAIN
NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION.
                                            NONHELICAL REGION (NC1).
                                                                                      /FTId=VAR_001838.
G -> R (IN SMCD).
/FTId=VAR_001839.
                                                                                                                                                 /FTId=VAR_001840.
C -> R (IN SMCD).
/FTId=VAR_001841.
                                                                           G -> E (IN SMCD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-105-1988 (Rel. 08, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Collagen alpha 1(X) chain precursor.
                                                                                                                                                                                                                                             33; Mismatches
                                                                                                                                                                                                                27.78;
                                                                                                                                                                                                                           36.88;
                                                                                                                                                                                                                                             86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
580
580
580
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19
19
57
545
18
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                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                              Best Local
Matches 8
                                                                                                                                    VARIANT
                                                                                                                                                                 VARIANT
                                                                         VARIANT
                                                                                                      VARIANT
CHAIN
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P08125;
                                DOMAIN
                                            DOMAIN
                                                         DOMAIN
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 GPRGPSGIPGVRGPIGPPGM--PGAPGAKGEAGAPGLPGPAGIVIKGLRGPMGPLGPPGP 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 AGLRRPHEGYEV-LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : : | ::|| ::| | ::| | 550 VILSKAYPGATVPIKFOYHVHAK---GINVWV 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLMKNGQVRASAIAQDADQ----NYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKY- 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 GPRGP-----GPDGAPASVPPFPPGAKGEVGRRG-----KAGLRGPP---GPPGP 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       491 KGNSGEPGLPGPPGPPGP-PGQSTIPEGYVKGESRELSGMSFMKAGANQALTGMPVSAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                 SUBUNIT: HOMOTRIMER.
PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEAU UNIT (G.Y-Y) ARE HYDROXYLAFED IN SOME OR ALL OF THE CHAINS.
SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01113; CiQ; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Cartilage; Collagen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.5%; Score 360.5; DB 1; Length 674;
3101. Chem. 264:16022-16029(1989). FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHOUNDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 1.3e-16;
31; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLLAGEN ALPHA 1(X) CHAIN.
NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
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EAB48B1EF174B145 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR, A31896; A31896. InterPro; IPRO01073; Clq.
InterPro; IPR000087; Collagen.
Pfam; PF001386; Clq; 1.
Pfam; PF001391; Collagen. 8.
PRINTS; PR00007; COMPLEMNTCIO.
SMART; SM00110; CLQ; 1.
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663 HSSFSGFL 670
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SIGNAL 1
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539
453
456
674 AA;
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MOD_RES
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SEQUENCE
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Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91113131; PubMed-1703407;
Thomas J.T., Kwan A.P.L., Grant M.E., Boot-Handford R.P.,;
"Isolation of cDMAs encoding the complete sequence of bovine type X
"collagen. Evidence for the condensed nature of mammalian type X
                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; 513301; 513301.

InterPro; IPR001073; C1q.

InterPro; IPR001087; Collagen.

Pfam; PF00386; C1q; InterPro; PF00386; C1q; InterPro; PF00386; C1q; InterPro; PF00386; C1q; InterPro; PF00387; Collagen; ProDon; PD00007; Collagen; InterPro; PF000110; C1q; InterPro; PF00110; C1q; InterPro; PF00110; C1q; InterPro; PF001113; C1q; InterPro; PF001113;
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HYDROXYLATION (BY SIMILARITY).

HYDROXYLATION (BY SIMILARITY).
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Best Local Similarity 36.8
Matches 88; Conservative
                                                                                                                                                                Bovidae; Bovinae; Bos.
Bos taurus (Bovine).
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674 AA;
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                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Cartilage;
                                                                                                                                                                                                                    NCBI_TaxID=9913;
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SEQUENCE
   SOLUTION TO THE TEST TO THE TE
"Amino acid sequence of the N-terminal 108 amino acid residues of the B chain of subcomponent Clq of the first component of human
                                                                                                                                                                                                                                                                                                                                                                    Reid K.B.M.;
"Moldecular cloning and characterization of the complementary DNA and gene coding for the B-chain of subcomponent Clq of the human complement system.";
Blochem. J. 231:729-735(1985).
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete amino acid sequences of the three collagen-like regions present in subcomponent Clq of the first component of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reid K.B.M., Gagnon J., Frampton J.; "Completion of the amino acid sequences of the A and B chains of subcomponent Clq of the first component of human complement."; Blochem. J. 203:559-569(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reid K.B.M., Bentley D.R., Wood K.J.; "Cloning and characterization of the complementary DNA for the chain of normal human serum Clq."; Philos. Trans. R. Soc. Lond., B, Biol. Sci. 306:345-354(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;.
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                        P02746; 096H17; 21-JUL-1986 (Rel. 01, Created) 01-JUL-1998 (Rel. 26, Last sequence update) 1-JUN-2002 (Rel. 41, Last annotation update) complement Clq subcomponent, B chain precursor.
                                                                                                            251 AA
                                                                                                              PRT;
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MEDLINE-82283890; PubMed-6981411;
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MEDLINE-98450587; PubMed-9777412;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-86076906; Pubmed-3000358;
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MEDLINE=79041552; PubMed=708376;
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MEDLINE-80020137; PubMed-486087;
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Biochem. J. 179:367-371(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 224-251 FROM N.A.
                                                                                                            STANDARD;
                                                                                                                                                                                                                                        Homo sapiens (Human)
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                                                                                                            C1QB_HUMAN
                 615
                                                                       RESULT 11
C1QB_HUMAN
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SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R AND S IN THE MOLAR RATION OF 1:2:2. C1Q SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE A ND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE C CHAIN.
                                                                         -!- PTM: O-LINKED GLYCANS CONSIST OF GLC-GAL DISACCHARIDES.
-!- DISEASE: DEFECTS IN CLOB ARE A CAUGE OF CLO DEFICIENCY. IT IS A RABE GENETIC DISORDER WHICH IS ASSOCIATED WITH RECURRENT INFECTIONS AND A HIGH PREVALENCE OF LUPUS ERYTHEMATOSUS-LIKE SYMPTOMS. IT IS CHARACTERIZED BY A LOSS OF ACTIVATION OF THE COMPLEMENT CLASSICAL PATHWAY.
-!- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydroxylation; Glycoprotein; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLEMENT C1Q SUBCOMPONENT, B CHAIN
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G -> D (IN C1Q DEFICIENCY).
/FTId-VAR_008541.
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N -> D (IN REF. 3).
G -> P (IN REF. 3 AND 4).
78C5752E267A0EF7 CRC64;
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EMBL; BC008983; AAH08983.1; ALF_INIT.
EMBL; M36278; AAC41692.1; -.
PIR; A03206; C1HUQB.
PIR; B23422; B23422.
Genew; HOMC:142; C1QB.
MIN; 120570; -.
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InterPro; IPR000087; Collagen.
Pfam; PF01391; C1q; 1.
Pram; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1.
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Complement pathway; Plasma;
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                                                                                                                                                                                                                        -----GEVGRRGKAGLRGPPGPPGPPGEPGRPGPPGPPGP-GPGGVAPAAGYVP 108
                                                                                                                                                                                                                                                                                         RIAFYA-----GLRRPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLM 162
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Muragaki Y., Jacenko O., Apte S., Mattei M.-G., Ninomiya Y.,
Muragaki Y., Jacenko O., Apte S., Mattei M.-G., Ninomiya Y.,
Olsen B.R.;
The alpha 2(VIII) collagen gene. A novel member of the short chain
of collagen family located on the human chromosome 1.";
J. Biol. Chem. 266:7721-7727(1991).
The BIOL Chem. 266:7721-7727(1991).
The PROLINIA MAJOR COMPONENT OF THE DESCEMET'S MEMBRANE (BASEMENT MEMBRANE) OF CORREALE MOOTHELIAL CELLS.
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UNIT (G-X-Y) ARE HYDROXILATED IN SOME OR ALL OF THE CHAINS.
THENDRALL STRONG, TO ALPHA 1 TYPES VIII AND X COLLAGEBNS.
                                                                                                                             10 VLMLLLLIGLIDISQ---PQLSCTGPPAIPGIPGIPGTPGPDGQPGT----PGIKGEKG
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR001073; C19.
InterPro; IPR001073; C10.
Pfam; PF00386; C10; 1.
Pfam; PF01391; Collagen; 8.
SMART; SM00110; C10; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Collagen alpha 2(VIII) chain (Endothelial collagen) (Fragment).
COLBA2.
                                                    42;
26.8%; Score 352; DB 1; Length 251; 35.9%; Pred. No. 1.8e-16; Live 34; Mismatches 90; Indels
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                                               Conservative
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                         Best Local Similarity
Matches 93; Conserv
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P25067;
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Homo.
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                                                                                                                                                                                                                                   96;
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                                                                                                                C1Q.
: 22A261164754F771 CRC64;
                                           NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 PRIAFYAGLRRPHEGYE------
                                                                                                                                                                                    26.3%; Score 345; DB 1; 33.0%; Pred. No. 1.2e-15; tive 32; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-UUN-2002 (Rel. 41, Created)
15-UUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF329836; AAK17960.1; -.
EMBL; BC011699; AAH11699.1; -.
Genew; HGNC:14325; C1QTNF2.
InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; 1.
                                                                                                                                        60527 MW;
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                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
Cell adhesion; Collagen
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468
635
635
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                                           <1
12
469
500
635 AA;
                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Muscle;
                                                                                                                                                                                         Mar
Local S.L..
96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CQT2_HUMAN
                                                                                                                DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         72
                                                                                                                                                                                       Query Match
                        NON_TER
DOMAIN
                                                                      DOMAIN
                                                                                            DOMAIN
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DOMAIN
DISULFID
MOD_RES
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGNAL
                                                                                                                                                                                                                                        <u>:</u>
    10;
                                                                                                                                                                                                    205 NKHLAIGLVHNGQYRIRTF--DANTGNHDVASGSTILALKQGDEVWLQIFYSEQNGLFYD 262
                                                                                                                                                                                        57 KGEVGRRGKAGLRGPPGPPGPPGPPGEPGRPGPPGPPGPG-----PGGVAPAAGYVP 108
                                                                                                                                                                                                                              RIAFYAGLRR--PHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGD 166
                                                                                                                                                                                                                                                                  167 GTSMWADLMKNGQVRASAIAQDADQ-NYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTN 225
                                                                                                                                                               26 GRCRMVCDPHGPRG-PGPDGAPA-----SVPPFPPGA 56
                                                                                                                                                                                                                                       50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Rawakami B., Nagai K., Isogai T., Sugano S.; "NEDO human cDNA sequencing project.", Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                        COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sellar G.C., Blake D.J., Reid K.B.M.; "Characterization and organization of the genes encoding the A-, and C-chains of human complement subcomponent Clq. The complete derived amino acid sequence of human Clq."; Biochem. J. 274:481-490(1991).
                                                                                                                 Length 285;
                                                                                                                                   83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                    C1Q.
: 7E31FF9868D4EDFA CRC64;
                                                                                                               25.0%; Score 328; DB 1; 33.6%; Pred. No. 7.2e-15;
                                                                                                                                                                                                                                                                                                                                                                                P02747; Q96DL2; Q96H05;
21-JUL-1986 (Rel. 01, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
Complement C1q subcomponent, C chain precursor.
C1QG OR C1QC.
                                                                   RELATED PROTEIN 2
                                                                                                                                                                                                                                                                                                                                                                          245 AA.
                                                                            COLLAGEN-LIKE.
                                                                                                                                 86; Conservative 37; Mismatches
                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Monocytes;
MEDLINE-91174759; PubMed-1706597;
Pfam; PF01391; Collagen; 2.
PRINTS; PROMODO; COMPLEMNTC1Q.
SMART; SMO0110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
                                                                                               29952 MW;
                                                                                                                                                                                                                                                                                                        226 KY---STFSGFIIYPD 238
                                                                                                                                                                                                                                                                                                                  263 PYWTDSLFTGFLIYAD 278
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                               15
285
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                             285 AA;
                                                                                                              Query Match
Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                      Collagen; Signal.
                                                   16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                          C10C_HUMAN
                                                                                                                                                                                                                             109
                                                                                              SEQUENCE
                                                                           DOMAIN
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                                                 SIGNAL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular basis of hereditary Clq deficiency.";

Immunobiology 199:286-294(1998).

-!- FUNCTION: ClQ ASSOCIATES WITH THE PROENZYMES CIR AND CIS TO YIELD

-!- FUNCTION: ClQ ASSOCIATES WITH THE PROENZYMES CIR AND CIS TO YIELD

C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE

COLLAGEN-LIKE REGIONS OF ClQ INTERACT WITH THE CA(2+)-DEPENDENT

CIR(2)CLS(2) PROENZYME COMPLEX, AND EFFTCIENT ACTIVATION OF CI

TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF CLQ WITH THE

FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.

-!- SUBUNIT: Cl IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEXES.

OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE

A AND B CHAAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF

THE C CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Þ
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DISEASE: DEFECTS IN CLIQ ARE A CAUSE OF CLQ DEFICIENCY. IT IS IRARE GENETIC DISORDER WHICH IS ASSCIATED WITH RECURRENT INFECTIONS AND A HIGH PREVALENCE OF LUPUS ERYTHEMATOSUS-LIKE SYMPTOMS. IT IS CHARACTERIZED BY A LOSS OF ACTIVATION OF THE COMPLEMENT CLASSICAL PATHWAY.
SIMILARITY: CONTAINS I COLLAGENOUS DOMAIN.
SIMILARITY: CONTAINS I CLQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydroxylation; Glycoprotein; Collagen;
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COLLAGEN-LIKE.
                                                                                                                                                                                               "Complete amino acid sequences of the three collagen-like regions present in subcomponent Clq of the first component of human complement.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN (WITH OTHER C CHAIN).
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O-LINKED (GAL.
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InterPro; IPR000087; Collagen.
Pfam; PP00386; Cqq; 1.
Pfam; PP01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTCLQ.
SMART; SM00110; ClQ; 1.
COMPLEMENT PATONON 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98450587; PubMed=9777412;
[4]
SEQUENCE OF 29-122.
MEDLINE=80020137; PubMed=486087;
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                                                                                                                                                                                                                                                                                                                                                                              Biochem. J. 179:367-371(1979)
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PIR; S14351; S14351.
Genew; HGNC:1245; C1QG.
MIM; 120575; --
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63
71
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                                                                                                                                                             Reid K.B.M.;
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UNCTION
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                                                                                                                                                                                                                YAGLRRPHE---GYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTS 169
                                                                                                                                                                          99
                                                                                                                                                            2 VLLLLVAIPLLVHSSRGPAHYEMLGRCRMVCDPHGPRGPGPDG-----APASVPPFP--P 54
                                                                                                                                                                                                                                                                                                                                                                                                                                             "cDNA cloning and expression of a novel adipose specific collagen-like factor, apM1 (AdiPose Most abundant Gene transcript 1).";
                                                                                                                                                                                              170 MWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKYST
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                   protein)
(Gelatin-
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saito K., Tobe T., Minoshima S., Asakawa S., Sumiya J., Yoda M.,
                                                                                                                                                30;
                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Adipose tissue;
MEDIINE-96224171; PubMed-8619847;
Maeda K., Okubo K., Shimomura I., Funahashi T., Matsuzawa Y.,
Matsubara K.;
                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Adiponectin precursor (30 kDa adipocyte complement-related | ACRP30) (Adipose most abundant gene transcript 1) (apM-1)
APMI OR ACRESO OR GBP28.
                                                                                                                                  Length 245;
                                                                                                                                                97; Indels
                                               DEFICIENCY).
                                                                                                                      FA17117EB7ABFC12 CRC64;
                                                                                                                                  ; DB 1;
7.2e-15;
                                              G -> R (IN C10 D)
/FTId=VAR_008542
              O-LINKED (GAL.
                                                                                                                                                36; Mismatches
                    HYDROXYLATION
                           HYDROXYLATION
                                  HYDROXYLATION
                                        HYDROXYLATION
                                                                                                                                  24.9%; Score 327;
                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE-99196984; PubMed-10095105;
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                                                                                                                                                Conservative
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 230 FSGFIIYPD 238
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                                                                                                                                                                                                                                                                                                                                                                             (Human)
                                                          14
23
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245 AA;
                                                                                                                                         Similarity
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                                                                 CONFLICT
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CARBOHYD
                                                                                                                                   Query Match
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                                MOD_RES
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VARIANT
                                                           CONFLICT
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                    MOD_RES
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-:- FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMATORY RESPONSES THROUGH ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPAB SIGNALING THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED EXPRESSION OF ENDOTHELIAL ADHESTON MOLECULES. INVOLVED IN THE CONTROL OF FAT METABOLLSM AND INSULIN SENSITIVITY.
-:- SUBGELLULAR LOCATION: SECRETED IN PLASMA.
-:- SUBGELLULAR LOCATION: SECRETED IN PLASMA.
-:- DISEASE: Defects in ADMI are the cause of adiponectin deficiency, resulting in very low concentration of plasma adiponectin.
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                                                                                                                                                                                                                                       MEDLINE-99333693; PubMed=10403784; Schaeffler A., Orso E., Palitzsch K.D., Buechler C., Drobnik W., Schaeffler A., Schoelmerich J., Schmitz G.; Fuerst A., Schoelmerich J., Schmitz G.; The human apm-1, an adipocyte-specific gene linked to the family of TNF's and to genes expressed in activated T cells, is mapped to chromosome 14213-423, a susceptibility locus identified for familial combined hyperlibidemia (FCH)."; Biochem. Biophys. Res. Commun. 260:416-425(1999).
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Blood 96:1723-1732(2000).
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MEDIINE-2040368; PubMed-10982546;
MEDIINE-2040368; PubMed-10982546;
Uouchi IN. Kihara S., Arita Y., Okamoto Y., Maeda K., Kuriyama H.,
Hotta K., Nishida M., Takahashi M., Muraguchi M., Ohmoto Y.,
Nakamura T., Yamashita S., Funahashi T., Matsuzawa Y.;
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endochelial NF-kappaB signaling through a cAMP-dependent pathway.";
Circulation 102:1296-1301(2000).
Nakano Y., Shimizu N., Tomita M.; "Organization of the gene for gelatin-binding protein (GBP28)."; Gene 229:67-73(1999).
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Yokota T., Oritani K., Takahashi I., Ishikawa J., Matsuyama A.,
Ouchi N., Kihara S., Funahashi T., Tenner A.J., Tomiyama Y.,
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MEDLINE-21671103; PubMed-11812766;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib.sib.ch).
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  Decreased adiponectin plasma levels are associated with obesity
            insulin resistance, and diabetes type 2.

--- PHARMACEUTICAL: Adiponectin might be used in the treatment of diabetes type 2 and insulin resistance.

---- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.

--- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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InterPro: IPR001087; Collagen.
Pfam: PF00386; C1q: 1.
PRam: PF00381; Collagen. 1.
PRINTS: PR00007; COMPLEMNTC1Q.
SMART; SM00110; C1Q: 1.
PROSITE; PS01113; C1Q: 1.
HOTMONE; Collagen; Signal; Repeat; Hydroxylation; Plasma; Polymorphism; Disease mutation; Obesity; Diabetes mellitus.
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ALIGNMENTS

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-09-506-855-3
-09-336-536-4
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             version :
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Maximum Match 100%
Listing first 45 summaries
                                                                  protein search, using sw model
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Gapop 10.0 , Gapext 0.5
           GenCore (c) 1993
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1311
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length: 2000000000
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Match
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Maximum 1
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Sequence 294, Application US/09188930A
Patent No. 6155502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Steachan, Lorna
APPLICANT: Steamen, Matthew
APPLICANT: Steamen, Matthew
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION UNDER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SEQ ID NOS: 348
LENGTH: 294
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RESULT 2 US-08-463-911-7

Sequence

Sequence Sequence

US-07-609-716-65 US-08-475-411A-65

08-642-255-32

Sequence

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Query Match
Best Local Similarity 34.37
Matches 92; Conservative
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                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-140-804-3
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US-09-336-536-20
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Patent No. 6197930
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF LINFORMATION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
                                                                                                                                                    E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.30
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Pred. No. 6e-20;
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NAME: Granahan, Patriola
REGISTRATION NUMBER: 32,27
REFERENCE/DOCKET NUMBER: WH195-05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,911
Sequence 7, Application US/08463911
Patent No. 5869330
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.38;
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TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 7:
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Best Local Similarity 34.3%
Conservative
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                                                                                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton,
                                                                                                                                                                                                       Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-463-911-7
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                         Lexington
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APPLICANT: Leiby, K.
APPLICANT: MCKSY, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                        24.3%; Score 318; DB 4; L6 34.3%; Pred. No. 6e-20;
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Pred. No. 6e-20;
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EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SORTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
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LENGTH: 23
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                         |:||||: : | | : | | : | | 158 YYFAYHITVYMXD---VKVSLFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQ 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58; Gaps
                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Otsuka Pharmaceutical Co., Ltd.
APPLICANT: Otsuka Pharmaceutical Co., Ltd.
TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a
TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit
TITLE OF INVENTION: therefor
FILE REFERENCE: P98-51
CURRENT APPLICATION NUMBER: US/09/530,423
CURRENT FILING DATE: 2000-05-01
PRIOR PILING DATE: 1997-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.3%; Score 318; DB 4; Length 244; 34.3%; Pred. No. 6e-20; Live 36; Mismatches 82; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT. ORGANISM: Abdominal fat tissue from myoma uteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 VYGEGERNGLYADNDNSTFTGFLLYHD 242
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                                                                             214 LDG-GKVHG--GNTNKYSTFSGFIIYPD 238
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Patent No. 5869330
                                                                                                                                                                                                                     Sequence 1, Application US/09530423 Patent No. 6461821
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CITY: Lexington
STATE: Massachusetts
COUNTX: USA
IP: 02173
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 244
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Best Local Similarity 34.33
Matches 92; Conservative
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54 PGAKGEVGRRGKAGLRGP-----PGPPGPRGPPGEPGRPGPPGPPGPGPGPGVAPAA 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 GGDGTSMWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGG- 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 MKD---VKVSLFKKDKAVLFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQVYGDGDHNGL 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LLFLLILP--SHAEDDVTTTEELAPA-LVPPPKGTCAGWMAGIPGHPGHNGTPGR--DGR
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Sequence 2. Application US/09530423

Patent No. 6461821

GENERAL INFORMATION:
APPLICANT: Otsuar Pharmaceutical Co., Ltd.

TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a

TITLE OF INVENTION: therefor

TITLE OF INVENTION: therefor

FILE REFERENCE: P98-51

CURRENT FILIAN APPLICATION NUMBER: US/09/530,423

CURRENT FILIAN DATE: 2000-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.2%; Score 317.5; DB 2; Length 247; 34.7%; Pred. No. 6.7e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                     COMPUTER: IBM PC compatible
COMPUTER: PC-COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Abdominal fat tissue from myoma uteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32; Mismatches
                                                                                                                                                  PRIOR APPLICATION NUMBER: JP H9-297569
PRIOR FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 YADNVND-STFTGFLLYHD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 ---NTNKYSTFSGFIIYPD 238
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Best Local Similarity 36.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 34.7%
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-463-911-2
COMPUTER READABLE FORM:
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-- EGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAY 158
                                                                                                              77 PRGPPGEPGRPGPPGPPG----PGPGGVAPAAGYV---PRIAFYAGLRRPHEGYEVLRFD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 PSGNPGKYGYPGPSGPLGARGIPGIKGTKGSPGNIKDQPRPAFSAIRRNPPMGGNVVIFD 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 DVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLM-----KNGQVRASA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 TVIINQEEPYQNHSGRFVCTVPGYYYFTFQVL-----SQWEICLSIVSSSRGQVRRSL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 CRMVCDPHGPRG----PGPDGAPASVPPFPPGAKGEVG-----RRGKAGLRGPPGPPG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 IAQDADQN--YDYASNSVILHLDVGDEVFIKLDGGKVH---GGNTNKYSTFSGFIIYP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 HVLMRGGDGTSMWADLMKNGQVRASAIAQDADQNYD---YASNSVILHLDVGDEVFIKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 -- RYKOKHOSVFTVTROTTOYPEANALVRFNSVVTNPQGHYNPSTGKFTCEVPGLYYFVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 245;
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Patent No. 6197930

GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-94

CURRENT APPLICATION NUMBER: US/09/140,804

CURRENT FILING DATE: 1998-08-26

EARLIER FILING DATE: 1997-08-26

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
CURRENT FALICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER RIGHG DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEO for Windows Version 3.0
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                                                                                                                                                                         216 GGKVHGGNTNKYSTFSGFIIYPD 238
                                                                                                                                                                                                                  224 DYNGMVGIEGSNSVFSGFLLFPD 246
                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09140804 Patent No. 6197930
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Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-140-804-4
  113 YAGLRRPH--
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LENGTH: 247
TYPE: PRT
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                                                                                                                                                                       70 TGVPGAEGPRGFPGIQGRKGEPGEG-----AYVYRSAFSVGL----ETYVTIPNMPIRF 119
                                                                                                                                                                                                                  129 DDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAIAQD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 LLLLFLLALPLRSQASAG--CYGIPGM-----PGMPGAPGKDGHDGLQGPKGEPGIPAV 66
                                             83
                                                                   38 RGPG----PDGA----PASVPPFP----PGAKGEVGRRGKAGLRGPPGPPGF
                                                                                                                            84 PGRPGPPGPPG------PGPGGVAPAAGYVPRIAFYAGLRRPHEGYEV----LRF
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  Gaps
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                                                                                                                                                                                                                                                                                                      189 ADQNYDYASNSVILHLDVGDEVFIKLDG-GKVHG--GNTNKYSTFSGFIIYPD 238
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72; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 9e-20;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH195-05
TELECHOMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08463911
Patent No. 5869330
32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-nocompage SOFTWARP
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84; Conservative
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Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 530
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Matches
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22.9%;
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                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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LENGTH: 228
                                                                                                                                                                                                                                   LENGTH: 247
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                  JS-09-506-855-3
                                                                                                                                                                                                                                                                              US-09-506-855-3
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                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                        62 DGTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPQTPGRKGEPG------EA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 GGDGTSMWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGG- 222
                                                                                                                                                          PGAKGEVGRRGKAGLRGP-----PGPPGPRGPPGEPGRPGPPGPPGPGPGVAPAA 104
                                                                                                                                                                                                                   105 GYVPRIAFYAGLR-RPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 PGAKGEVGRRGKAGLRGP-----PGPPGPRGPPGEPGRPGPPGPPGPPGPGCVAPAA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 GYVPRIAFYAGLR-RPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LLLLVAIPLLVHSSRGPAHYEMLGRCRMVCDPHG------PRGPGPDGAPASVPPFP 53
                                                                                                                                 61
                                                                                                                    || || : :| |:
|LFLLILP--SHAEDDVTTTEELAPA-LVPPPKGTCAGWMAGIPGHPGHNGTPGR--DGR
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                                                                          Gaps
                                                                        43;
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                                             Length 247;
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                                                                        95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
                                          23.6%; Score 309.5; DB 4; 34.4%; Pred. No. 3.3e-19; 11ve 32; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 3.3e-19; 32; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.6%; Score 309.5; 34.4%; Pred. No. 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/118,408A CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,154
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3 LENGTH: 247
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09118408A Patent No. 6265544
                                                                                                                                                                                                                                                                                                                                                    223 ---NTNKYSTFSGFIIYPD 238
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                                        Query Match 23.6%
Best Local Similarity 34.4%
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 34.48
Matches 89; Conservative
; ORGANISM: Homo sapiens US-09-140-804-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 GYVPRIAFYAGLR-RPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 GGDGTSMWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGG- 222
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Patent No. 6406684

GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: BOSSONE, S.
TILE REFERENCE: 7853-144

CURRENT APPLICATION: SOME 1999-06-18

CURRENT ELING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 75

SOFTWARE: Patentin Ver. 2.0
                                                          APPLICANT: Sheppard, Paul O.
APPLICANT: Lasser, Gerald W.
APPLICANT: Lasser, Gerald W.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND FITLE OF INVENTION: IMMUNE FUNCTION
FILLE REFERENCE: 99-12
CURRENT APPLICATION NUMBER: US/09/506,855
CURRENT APPLICATION NUMBER: US/09/506,855
CURRENT FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FASTERO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                23.6%; Score 309.5; DB 4; 34.4%; Pred. No. 3.3e-19;
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1.9e-18;
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Pred. No. 1
Sequence 3, Application US/09506855 Patent No. 6448221 GENERAL INFORMATION:
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228 YADNVND-STFTGFLLYHD 245
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                 ---GPGGVAPAAGYVPRIAFYA---GLRRPHEGYEVLRFDDVVTNVGNAYEAASGKFTCP 149
                                                    72 GPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQ 131
                                                                                         MPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAIAQDADQNYDY-----ASNSV 200
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                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 243;
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APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                 201 ILHLDVGDEVFIKLDGGKVHG--GNTNKYSTFSGFIIYPD 238
                                                                                                                                                                                        201 ILHLDVGDEVFIKLDGGKVHG--GNTNKYSTFSGFIIYPD 238
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; Pred. No. 2.1e-18;
27; Mismatches 78
                                                                                                                                                                                                                                                                                               Sequence 295, Application US/09188930A Patent No. 6150502 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09140804
Patent No. 6197930
GENERAL INFORMATION:
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36.8%;
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Best Local Similarity
Matches 81; Conserva
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Sequence 118, App
Sequence 119, App
Sequence 3, Appli
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Sequence 2, Appli
Sequence 2, Appli
Sequence 42, Appli
Sequence 362, Appli
Sequence 363, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 DGTSMWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTN
                                        Sequence 115,
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                           Sequence
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 sequence
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Patent No. US20020160474A1

GENERAL INFORMATION:

APPLICANT: FOX, Brian

TITLE OF INVENTION: ADIPOCYTE COMPLEMENT RELATED PROTEIN

TITLE OF INVENTION: AZCRP11

FILE REFERENCE: 00-91

CURRENT APPLICATION NUMBER: US/09/998,582

CURRENT FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: US 60/253,863

PRIOR FILING DATE: 2000-11-29

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 3.0
          US-09-789-561-154
US-09-780-561-154
US-09-800-729-115
US-09-800-729-115
US-09-800-729-115
US-09-800-729-119
US-09-800-729-119
US-09-911-176B-3
US-10-180-762-3
US-09-944-413-42
US-09-944-413-42
US-09-944-403-42
US-09-944-907-42
US-09-944-917-918-362
US-10-123-904-362
US-10-123-904-362
US-10-123-904-362
US-10-123-904-362
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US-10-123-904-362
US-10-175-74-362
US-10-175-74-362
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3; Pred. No. 1.5e-38;
15; Mismatches 40,
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              Query Match
Best Local Similarity 58.8%
Matches 144; Conservative
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SEQ ID NO 2
LENGTH: 268
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Sequence 48, Appl
Sequence 51, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 116, Appli
Sequence 116, Appli
Sequence 116, Appli
Sequence 116, Appli
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Sequence 2, Appli
Sequence 382, App
Sequence 294, App
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                                                                                                             (without alignments)
1147.202 Million cell updates/sec
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                                                                                                                                                                             1 MVLLLLVAIPLLVHSSRGPA.......VHGGNTNKYSTFSGFIIYPD
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/ cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep: *
/ cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep: *
/ cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep: *
/ cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep: *
/ cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep: *
/ cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep: *
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep: *
/ cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep: *
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep: *
/ cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep: *
/ cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep: *
                                                                                           June 2, 2003, 16:46:45; Search time 21 Seconds
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-001-887-108
US-10-219-449-4
US-10-219-449-2
US-09-866-050A-382
US-09-866-050A-294
US-09-866-050A-294
US-09-866-050A-630
US-09-8611-176B-48
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US-09-788-055-6
US-09-909-547-6
US-09-776-976-4
US-09-758-055-4
US-09-909-547-4
US-09-9000-729-116
US-09-911-1768-49
                                                                                                                                                                                                                                                                          Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                 383519 seqs, 101223694 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                      Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                             US-10-005-499-378
1311
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Match
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662.5
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318.3
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318.3
318.3
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Perfect score:
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236 YP 237
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SEQ ID NO 40
LENGTH: 744
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                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chao, Yumei
APPLICANT: Chao, Xumei
APPLICANT: Monahan, John
APPLICANT: Kanaetkar, Shubhangi
APPLICANT: Sanatkar, Shubhangi
APPLICANT: Gatt, Karen
APPLICANT: Ganavarapu, Manjula
APPLICANT: Gornavarapu, Manjula
APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 SVPPFPPGAKGEVGRRGKAGLRGPPGPPGPRGPPGEPGRPGPPGPPG
                                                                                                             Sequence 2, Application US/09998563

Patent No. US/20020155546A1

REBERAL INFORMATION:
APPLICANT: FOX, BEIAN
TITLE OF INVENTION: ADIPOCYTE COMPLEMENT RELATED PROTEIN
TITLE OF INVENTION: ADARP12
FILE REFERENCE: 00-93
CURRENT APPLICATION NUMBER: US/09/998,563
CURRENT FILING DATE: 2000-11-16
PRIOR FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR PRICATION NUMBER: US 60/298,155
PRIOR PLILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
SUNBER OF SEQ ID NOS: 238
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 4
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 250
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen, Yan
Zhao, Xumei
Monahan, John
Kamatkar, Shubhangi
Glatt, Karen
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11111
210 KYSTF 214
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APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and
FILE REFERENCE: DEX. 2069
CURRENT APPLICATION NUMBER: US/10/001,887
CURRENT FILING DATE: 2001-11-20
                                                                                                                                   10;
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                                                                                                                                                                                                                                                                  93 PG-PGPGGV-----APAAGYVPRIAF-YAGLRRPH-------EGYEV-----125
                                                                                                                                                                                                                                                                                                126 -----LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKN 177
                                                                                                                                                                                                                                                                                                                                                                                   625 PFPPVGGPVKFNKLLYNGRQNYNPQTGIFTCEVPGVYYFAYHVHCKGG---NVWVALFKN 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 GQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKY--STFSGFII 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           682 NEPVMYTYDEYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHSSFSGYLL 741
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                                                                                       Length 744;
                                                                                                                                   77; Indels
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                                                                                   28.7%; Score 376; DB 9; 37.2%; Pred. No. 2.6e-18; ive 31; Mismatches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-001-887-108
; Sequence 108, Application US/10001887
; Patent No. US20020155464A1
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PRIOR APPLICATION NUMBER: 60/249,998
PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/252,563 PRIOR FILING DATE: 2000-11-22
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SOFWARE: Patentin version 3.1
SEQ ID NO 108
LENGTH: 638
                                                                                                            Best_Local Similarity 37.2%
Matches 90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
TYPE: PRT
ORGANISM: Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapien US-10-001-887-108
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Best Local Similarity
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473 RGPSGIPGL------QGPAGPIGPQGLPGLKGEPGLPGPPGE-GRAGEPGPTGP 522
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                                                                                                                          Length 717;
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                                                                                                                                                                 77; Indels
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APPLICANT: Murison, James G.
APPLICANT: Mumble, Firshanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 24.9%; Score 327; DB 9; I
Best Local Similarity 32.7%; Pred. No. 2.3e-15;
Matches 86; Conservative 33; Mismatches 80;
                                                                                                                      26.4%; Score 345.5; DB 9 35.6%; Pred. No. 3.1e-16; Live 30; Mismatches 77
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CURRENT APPLICATION NUMBER: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
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693 SDQANGLYSTEYIHSSFSGFLLCP 716
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                                                                                                                                                              94; Conservative
                                      ; TYPE: PRT
; ORGANISM: homo sapiens
US-10-219-449-2
                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Rat
US-09-866-050A-382
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SEQ ID NO 382
SEQ ID NO 2
LENGTH: 717
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Publication No. US20030077820A1
GENERAL INFORMATION:
APPLICANT: Xie, Qiongshu
APPLICANT: No. US20030077820A1e1 Human Collagen Proteins and Polynucleotides
FILE REFERENCE: LEX-0363-USA
CURRENT APPLICATION NUMBER: US/10/219,449
PRIOR APPLICATION NUMBER: US 60/312,300
PRIOR APPLICATION NUMBER: US 60/312,300
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                  APPLICANT: Xie, Glongshu
APPLICANT: Hu, Yi
TITLE OF INVENTION: NO. US20030077820Alel Human Collagen Proteins and Polynucleotides
FILE REFERENCE: LEX-0363-USA
CURRENT APPLICATION NUMBER: US/10/219,449
PRIOR FILING DATE: 2002-08-14
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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               AYHVLMRGGDGTSMWADLMKNGQVRASAIAQDADQNY-DYASNSVILHLDVGDEVFIKLD 215
                                    ...-----VLRFDDVVTNVGNAYEAASGKFTCPMPGVYFF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     563 QFGLGELSAHATPAFTAVLTSPFPASGMPVKFDRILYNGHSGYNPATGIFTCPVGGVYYF 622
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AYHVHVK---GTNVWYVALYKN-NVPATYTYDEYKKGYLDQASGGAVLQLRPNDQVWVQMP 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGPRGPPGEPGRPGPPGPPGPGGVAPAAGYVPRIAFYAGLRRPHEGYE------ 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63;
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                                                                                                                      614 SDQANGLYSTEYIHSSFSGFLLCP 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDQANGLYSTEYIHSSFSGFLLCP 702
                                                                                          216 GGKVHGGNTNKY--STFSGFIIYP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 GGKVHGGNTNKY -- STFSGFIIYP 237
                                                                                                                                                                                                                                     Sequence 4, Application US/10219449
Publication No. US20030077820A1
GENERAL INFORMATION:
APPLICANT: Yu, Xuanchuan (Sean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4
LENGTH: 703
                                                                                                                                                                                                 RESULT 5
US-10-219-449-4
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 630
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                                                                                                                                                Query Match
Best Local Similarity
Matches 92; Conserv
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Best Local Similarity
                                                                                                         US-09-866-050A-630
                                                                                      ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-911-176B-48
                                . 289
PRT
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201 ITLA---NKHLAIGLVHNGQYRIRTF--DANTGNHDVASGSTILALKEGDEVWLQIFYSE 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 KGEVGRRGKAGLRGPPGPPGPPGEPGRPGPPGPPGP----GPGGVAPAAGYVPRIA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 VIMRGGDGTSMWADIMKNGQVRASAIAQDADQ-NYDYASNSVILHLDVGDEVFIKLDGGK 218
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                                                                                                                                                                                                                                          APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Orrust, Rene
APPLICANT: Orrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFRENCE: 11000.1011c4U
CURRENT APPLICATION NUMBER: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
TITLE OF INVENTION: Compositions isolated From Skin Cells;
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c4U
CURRENT APPLICATION UNMERR: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 24.9%; Score 327; DB 9; Best Local Similarity 32.7%; Pred. No. 2.4e-15; Matches 86; Conservative 33; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 GRCRMVCDPHGPRG-PGPDGAPASV----
                                        219 VHGGNTNKY---STFSGFIIYPD 238
                                                            219 VHGGNTNKY---STFSGFIIYPD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 QNGLEYDPYWTDSLFTGFLIYAD 287
                                                                                                                                                                                    Sequence 294, Application US/09866050A Publication No. US20030040471A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ORGANISM: Rat
US-09-866-050A-294
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                                                                                                                                                                                                                                                                                                                                                            141 AASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAIAQDADQ-NYDYASNS 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 YFFAYHVLMRGGDGTSMWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIK 213
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                                                                                                                                  1 MIVLLYVISLAICASGOPRGNOAKGESYSPRYICSIPGLPGPPGPPGANGSPGPHGRIGL 60
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                                                                                                                                                                                 53 ----PPGAKGEVGRRGKAGLRGPPGP------PGPRGPPGEPGRPGPPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LLLLVAIPLLVHSSRGPAHYEMLGRCRMVCDPHGPRGPG----PDGA----PASVPPFP
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Length 289;
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Sequence 48, Application US/09911176B
Patent No. US20020156243A1
GENERAL INFORMATION:
TITLE OF UNVENTION: ANTIBODIES THAT BIND AN
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG
FILE REFERENCE: 97-30D1
CURRENT APPLICATION NUMBER: US/09/911,176B
CURRENT APPLICATION NUMBER: 09/118,408
PRIOR APPLICATION NUMBER: 09/118,408
PRIOR APPLICATION NUMBER: 60/053,154
PRIOR FILING DATE: 1998-07-17
PRIOR FILING DATE: 1997-07-18
                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                200 VILHLDVGDEVFIKL---DGGKVHGGNTNKYSTFSGFIIYPD 238
DB 9;
                                            35; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.3%; Score 318; DB 9; 34.3%; Pred. No. 8.2e-15;
                       .6e-15
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24.4%; Score 319.5; 32.6%; Pred. No. 7.6
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 48
LENGTH: 244
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PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR PELICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent.pm
                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-776-976-6
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US-09-758-055-6
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Best Local Similarity
                                                                                                                                                                                        LENGTH: 244
                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                     SEQ ID NO 6
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APPLICANT: Fruebis, Joachim
APPLICANT: Yen, Frances
APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
CURRENT APPLICATION NUMBER: US/09/776,976
CURRENT APPLICATION NUMBER: 2001-02-05
                                                                                                                                                                       Sequence 51, Application US/10180762
Fublication No. US20030022838A1
GENERAL INRORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Lasser, Gerald W.
APPLICANT: Lasser, Gerald W.
TILE OF INVERTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE FUNCTION
FILE REFERENCE: 99-12C3
CURRENT APPLICATION NUMBER: US/10/180,762
FRIOR APPLICATION NUMBER: 09/253,604
FRIOR APPLICATION NUMBER: 09/253,604
FRIOR APPLICATION NUMBER: 09/2444,794
FRIOR FILING DATE: 1999-11-22
FRIOR FILING DATE: 1999-11-22
FRIOR FILING DATE: 1999-11-22
SPRIOR FILING DATE: 1000-02-17
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 YFFAYHVIMRGGDGTSMWADIMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIK 213
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  158 YYFAYHITVYMKD---VKVSLFKKDKAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQ 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 244;
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24.3%; Score 318; DB 9; Length 24
Best Local Similarity 34.3%; Pred. No. 8.2e-15;
Matches 92; Conservative 36; Mismatches 82; Indels
                                                               214 LDG-GKVHG--GNTNKYSTFSGFIIYPD 238
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Patent No. US20020037849A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-10-180-762-51
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Sequence 6, Application US/09758055

Patent No. US20020056617A1

GENERAL INFORMATION:

APPLICANT: Fruebis, Joachim

APPLICANT: Erickson, Mary Ruth

APPLICANT: Elickson, Mary Ruth

APPLICANT: Elickson, Mary Ruth

APPLICANT: Elickson, Mary Ruth

APPLICANT: Elickson, Mary Ruth

APPLICANT: 2001, Bernacd

FILE REFERENCE: 76.US4.REG

CURRENT APPLICATION NUMBER: US, 60/176, 228

PRIOR FILING DATE: 2000-01-14

PRIOR FILING DATE: 2000-04-13

PRIOR FILING DATE: 2000-04-13

PRIOR APPLICATION NUMBER: US 60/198,087

PRIOR FILING DATE: 2000-04-13

PRIOR APPLICATION NUMBER: US 60/299,881

PRIOR APPLICATION NUMBER: US 60/299, RB1

PRIOR APPLICATION NUMBER: US 60/299, RB1

SEGTWARE: PATENT PATENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98
                                                                                                                                                                                                                                  1 MLLLGAVLLLLAL---PGHDQ------ETTTQGPGVLLPLPKGACTGWAGIPGHP 47
                                                                                                                                                                                                                                                                                                                                                                                                                     54 -----PGAKGEVGRRGKAGLRGPPGPPGPPGEPGRPGPPGPPGPPG------PGPG
                                                                                                                                                                                   3 LLLLVAIPLLVHSSRGPAHYEMLGRCRMVCDPHGPRGPG----PDGA----PASVPPFP
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    Length 244;
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                                                                                         Indels
Query Match 24.3%; Score 318; DB 10; Best Local Similarity 34.3%; Pred. No. 8.2e-15; Matches 92; Conservative 36; Mismatches 82;
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Pred. No. 8.2e-15;
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34.3%;
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Mass

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APPLICANT: Erickson, Mary Ruth
APPLICANT: Erickson, Mary Ruth
APPLICANT: Yen, Frances
APPLICANT: Bilain, Bernes
APPLICANTON: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
CURRENT PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/776,28
PRIOR APPLICATION NUMBER: US 60/176,28
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 DGTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPG------EA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 GYVPRIAFYAGLR-RPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMR 163
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Job time: 23 secs
                                           Sequence 4, Application US/09776976
Patent No. US20020037849A1
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APPLICANT: Elickson, Mary Ruth
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass;
FILE REFERENCE: 76.026.CIP
CURRENT APPLICATION NUMBER: US,09/909,547
CURRENT FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/758,055
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 7
                                                                                                               -----AYVRSAFSVGL----ETYVTIPNMPIRFTKIFYNQONHYDGSTGKFHCNIPGL 157
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                                        48 GHNGAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIOGRKGEPGEG 107
                                                                                                                                                                       154 YFFAYHVLMRGGDGTSMWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIK 213
                                                                                                                                                                                                -----AYVRSAFSVGL----ETXVTIPNMPIRFTKIFYNQONHYDGSTGKFHCNIPGL 157
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8.2e-15;
                                                                                                                                                                                                                                                             214 LDG-GKVHG--GNTNKYSTFSGFIIYPD 238
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34.3%; Pred. No. 8
tive 36; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09909547
Patent No. US20020091080A1
GENERAL INFORMATION:
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Matches 92; Conservative
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104

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Length 247; Indels 227

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 2, 2003, 16:43:09; Search time 18 Seconds (without alignments) 1271.111 Million cell updates/sec Run on:

US-10-005-499-378
1311
1 MVLLLLVAIPLLVHSSRGPA.....VHGGNTNKYSTFSGFIIYPD 238 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

283224 Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Query Match 29.7%; Score 389; DB 1; Length 743;	Matches 94; Conservative 30; Mismatches 77; Indels 46; Gaps 10;		OY 31 VCDPHGPRGPGPDGAPASVPPPPGAKGEVGRKGKAGLRGPPGPPGEPGR 86		DD 502 IVGPSGPIGPPGIPGPKGEPGLPGPPGFPG-VGKPGVAGLHGPPGKPGALGPQGQPGL 558		OV 87 PGPPGPPG-PGPGGVAPAAGYVPRIAFYAGLRRPHEGYEV 125		GIDGVKTPH		Qy 126LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWA 172		DD 619 AELTVPFPPVGAPVKFDKLLYNGRQNYNPQTGIFTCEVPGVYYFAYHVHCKGGNVWV 675		Qy 173 DLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKYSTF 230		Db 676 ALFKNNEPMMYTYDEYKKGFLDQASGSAVLLLRPGDQVFLQNPFEQAAGLYAGQYVHSSF 735		Ov 231 SGFIIYP 237		Db 736 SGYLLYP 742			RESULT 2	A34246	collagen alpha 1(VIII) chain precursor - rabbit	C;Species: Oryctolagus cuniculus (domestic rabbit)	C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999	C; Accession: A34246	R; Yamaquchi, N.; Benya, P.D.; van der Rest, M.; Ninomiya, Y.	J. Biol. Chem. 264, 16022-16029, 1989	A;Title: The cloning and sequencing of alphal(VIII) collagen cDNAs demonstrate that t	
		Description		collagen alpha 1(V	collagen alpha 1(V	alpha 1	alpha 1	alpha 1	alpha 1	_	_	ដ	collagen alpha 2(v	complement subcomp	gelatin-binding 28	complement subcomp	complement protein	complement subcomp	complement Cld B c	complement subcomp	hypothetical prote	hibernation-relate	hibernation-relate	hypothetical prote	collagen precursor	cerebellin-like ql	cerebellin precurs	hibernation-relate	collagen II Al pro	collagen alpha 1(I	ซ	collagen alpha 1(I	
SUMMARIES	Query	No. Score Match Length DB ID		29.7 743 1 8	29.6 744 1	29.3	680 2	28.7	28.2 674 2	27.7 680 1	27.5 674 2	26.8 253 1	10 345 26.3 635 2 A57131	24.6 245 1	24.3 244 2	24.1	24.1 253 2	24.0 245 1	23.3 253 2	23.0 245 2	22.9 219 2	20.5	215 2	19.9 992 2	19.1 423 2	18.5 224 2 1	17.5 193 2	196 2	464 2 3	_	473 2	_	

16.1 1466 1 CCHU7L COllagen alpha 1(I 1492 2 A40333 COllagen alpha 1(I 1492 2 A40333 COllagen alpha 1(I 15.9 453 2 S18804 COllagen alpha 1(I 15.9 453 2 S18804 COllagen alpha 1(I 15.8 1315 2 A56101 COllagen alpha 1(X 15.8 1774 2 B56101 COllagen alpha 1(X 15.8 1774 2 B56101 COllagen alpha 1(X 15.8 1419 2 A41182 COllagen alpha 1(I 15.8 1419 2 A41182 COllagen alpha 1(I 15.6 677 2 S23296 COllagen alpha 1(I 15.6 677 2 S23296 COllagen alpha 1(I 15.6 170 2 B57131 COllagen alpha 1(I 15.6 170 2 B57131 COllagen alpha 2(I 15.6 170 2 B57131 COllagen alpha 2(I 15.6 170 2 B57131 COllagen alpha 1(I 15.5 170 2 B57131 COllagen alpha 1(I 15.5 170 2 B34770 COllagen alpha 1(V 15.5 102 2 B34770 CORPZ protein - sai	· ALIGNMENTS	RESULT 1 S23779 Collagen alpha 1(VIII) chain - mouse Collagen alpha 1(VIII) chain - mouse C. Species: Mas musculus (house mouse) C. Species: Mas musculus (house) C. Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 C. Accession: 23779 EM. 2377	LLLRPGDQVFLQNPFEQAAGLYAGQYVHS
211 210.5 208.5 208.5 207.5 207.5 206.5 206.5 206.5 206.5 208.5 208.2 208.2		1 a alpha 1 b ses: Mus n 10-Sep. 10-Se	676 AI
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT 1 \$23779 collagen alpha 1(VIII) C;Species: Mus musculus C;Date: 10-Sep-1999 #se C;Accession: 523779 R;Muragaki, Y.; Shiota, Eur. J Biochem. 207, 8 A;Title: Alpha-1(VIII) A;Reference number: 523 A;Accession: 523779 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-743 < MURA A;Resid	qq

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172 ADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKY--ST 229
                                                                                                            |||:::||
FSGYLLYP 743
                                                                                  230 FSGFIIYP 237
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C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S23298
C;Accession: S23298
R;Ninomiya, Y; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; McC maguchi, N.; Olsen, B.R.
M: Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pre A;Title: The molecular biology of collagens with short triple-helical domains.
                                                                                                 A;Cross-references: GB:J05042; NID:g164895; PIDN:AAA31204.1; PID:g164896
C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology
E;1-20/Domain: signal sequence #status predicted <SIG>
F;21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
F;21-117/Region: amino-terminal nonhelical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-744 <NIN>
C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology
F;617-743/Domain: complement Clq carboxyl-terminal homology <ClQ>
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                                                                                                                                                                                                                                                                                                                                                                                          PGPPGPPG-PGPGGV-----APAAGYVPRIAF-YAGLRRPH-------EGYEV---
                                                                                                                                                                                                                                                                                                                                                                     31 VCDPHGPRG----PGPDGAPASVPPFPPGAKGEVGRRGKAGLRGPPGPPGPPGFPGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 VCDPHGPRG----PGPDGAPASVPPFPPGAKGEVGRRGKAGLRGPPGPPGPPGEPGR
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                             47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
                                                                                                                                                                                                                                                                                      DB 1; Length 744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 744;
                                                                                                                                                                                                 F;118-571/Region: interrupted helical
F;572-744/Region: carboxyl-terminal nonhelical
F;617-743/Domain: complement Ciq carboxyl-terminal homology <ClQ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3e-20;
------ 79; Indels
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGPPGPPG-PGPGGV----APAAGYVPRIAF-YAGLRRPH----
omains similar to those of type X collagen.
A;Reference number: A34246; MUID:89380199; PMID:2476437
A;Accession: A34246
                                                                                                                                                                                                                                                                                          3.4e-21;
78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                    Similarity 37.5%; Pred. No. 5.4e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 383.5;
; Pred. No. 1.3e
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collagen alpha 1(VIII) chain - chicken
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FSGYLLYP 743
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Best Local Similarity
Matches 93; Conserv
                                                                                A; Residues: 1-744 <YAM>
                                                             A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S23298
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                             93;
                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 93)
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collagen alpha 1(X) chain precursor - mouse
C; Species: Mus musculus (house mouse)
C; Species: J0-Sep-1993 #text_change 13-Aug-1999
C; Dates 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C; Accession: S31216; S28807; S2215; S30127; I48299; S26397; S31830
R; Kong, R. Y. C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E. Eur. J. Blochem. 213, 99-111, 1993
A; Title: Intron-exon structure, alternative use of promoter and expression of the mou A; Reference number: S31216; MUID:93238750; PMID:8477738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: collagen alpha l(VIII) chain; complement Clq carboxyl-terminal homolog C; Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer F;1-18-Domain: signal sequence *status predicted <SIG> F;19-680/Product: collagen alpha l(X) chain *status predicted <MAT> F;553-679/Domain: complement Clq carboxyl-terminal homology <ClQ>
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A; Modecule type: mRNA
A; MANA
A; Modecule type: MRNA
A; MANA
A; Modecule type: MRNA
A; MANA
A; Modecule type: MRNA
A; Modecule type: MRN
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A; Residues: 1-680 <RON>
A; Ross-references: EMBL:221610; NID:949793; PIDN:CAA79736.1; PID:949794
A; Cross-references: EMBL:221610; NID:949793; PIDN:CAA79736.1; Peraelae, M.; de Biochem. J. 289, 247-253, 1993
Biochem. J. 289, 247-253, 1993
A;Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and A; Reference number: $28807; MUID:93143676; PMID:8424763
A; Accession: $28807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-285, A, 287-680 < ELI>
A; Residues: 1-285, A, 287-680 < ELI>
A; Cross-references: EMBL:X67348; NID:950480; PIDN:CAA47763.1; PID:950481
R; Elima, K.; Metsaeranta, M.; Kallilo, J.; Peraelae, M.; Eerola, I.; Garofalo, S.; de Blochim. Blophys. Acta 1130, 78-80, 1992
A; Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen A; Reference number: $22215; MUID:92182017; PMID:1543751
A; Accession: $22215
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A:Molecule type: mRNA
A:Cross-references: BMBL:X63013; NID:949795; PIDN:CAA44741.1; PID:949796
B:Apte, S.S.; Olsen, B.R.
Matrix 13, 165-179, 1993
A:Title: Characterization of the mouse type X collagen gene.
A:Reference number: S30127; MUID:93261348; PMID:8492743
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A; Residues: 'SDGYFSQ', 24-26, 'KQ' <SUM>
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us-10-005-499-378.rpr

Ouery Match Best Local Similarity 37.4%; Pred. No. 4e-20; Matches 91; Conservative 31; Mismatches 77; Indels 44; Gaps 9;	Qy 236 YP 237 11 Db 742 YP 743
Qy 36 GPRGPGPDGAPASVPPFPPGAKGEVGRRGKAGLRGPPGPPG 79	RESULT 6 S23297 collagen alpha 1(X) chain precursor - chicken
OY 80 PPGEPGRPGPPGPGGGVAPAAGYVPRIAFYAGLR 117	N;Alternate names: type X collagen C;Species: Gallus gallus (chicken) C;Date: 07-0ct-1994 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999 C:Accession: S23297; A31896; S65594: S7771: 150218
118 RPHEGYEV-LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAXHVLMRGGDGTSMWADLMK 176	Rivinomisa Y.; Caramana, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; maquchi, N.; Olsen, B.R.
616	in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic A;Title: The molecular biology of collagens with short triple-helical domains.
QY 177 NGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKYSTFSGFI 234	A; Accession: \$23297 A; Status: preliminary A; Molecule type: mRNA
Oy 235 IYP 237	A; Residues: 1-674 <nin> R:LuValle, P.; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R. J. Riol, Chem. 263, 1878-18385, 1988</nin>
Db 677 VAP 679	A; Title: The type X collagen gene. Intron sequences split the 5'-untranslated region A; Reference number: A31896; MUID:89054019; PMID:2461368
RESULT 5 S15435	A; Molecule type: mRMA: A; Molecule type: mRMA: A; Residues: 1-75 -ct.IIV>
	R:Ninomiya; Y.; Gordon, M.; van der Rest, M.; Schmid, T.; Linsenmayer, T.; Olsen, B.R. J. Biol. Chem. 261, 5041-5060, 1986
. 1999	A: Title: The developmentally regulated type X collagen gene contains a long open read A:Reference number: 15(7)18: MITD: 86168277: PMID: 3(82876
	A.ACCESSION: S65594 A.MOISTING THE TOTAL OF
in and assignment	A.RESIGUES: 'T', 9, 'D', 11-12, 'EDQMKLYILETM', 30-31, 'TCKSGRAFTTWILQNVMADLVSSHT', 48-89,' 629, 'PQAVLSLISWRTIKCGSSCQIQNPWVSIPLNMFILLSQVSYLLKSNNIPLTMS' <nin1></nin1>
	A;Cross-references: EMBL:M13496; NID:g211699; PIDN:AAA48736.1; PID:g211700 A;Accession: S77711 A;Monal + mon. material
82	A, moreorize types 104-112, /X, 114-117;453-466 <nin2> C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homolog</nin2>
	C.Keywords: coiled coil; extracellular matrix; diycoprotein; homotrimer; hydroxyproli F;1-18/Domain: signal sequence #status predicted <sig> F;547-673/Domain: complement Ciq carboxyl-terminal homology <ciq></ciq></sig>
erminal homology	F;453,456/Modified site: hydroxyproline (Pro) #status experimental F;611/Binding site: carbohydrate (Asn) (covalent) #status predicted
	Query Match 28.2%; Score 369.5; DB 2; Length 674;
21-11/7 KEG101 118-571/Regid 572-744/Regid	Best Local Similarity 36.7%; Pred. No. 1.2e-19; Matches 91; Conservative 32; Mismatches 66; Indels 59; Gaps 10;
F;617-743/Domain: complement C1q carboxyl-terminal homology <c1q></c1q>	Qy 36 GPRGPGPDGAPASVPPFPPGAKGEVGRRGKAGLRGPPGPPGP 77
28.7%; Score 376; DB 2 37.2%; Pred. No. 4.4e-2	PSGIPGIRGPIGPPGMPGAPGAKGEAGAPGLPGPAGIATKGLRGPM
Matches 90; Conservative 31; Mismatches 77; Indels 44; Gaps	78 RGPPGEPGRPGPPGPGGVAPAAGYVPRIAFY :
OY 34 PHGPRG-PGPDGAPASVPPFPBGAKGEVGRRGKAGLKGPPGPPGPPGPPGPPGPPGP 92	491 KGNSGEPGLPGPPGPP-PGQSTIPEGYVKGESRELSGMSFMKAGANQALTGMPVSAFT
86	VY 114 AGLEKRYELEN LEKEDDVILVORNIEARAGNETCEMENVERFRATRYLMRUGUGIDAMA 1/2
: IGAKKGKNGGPAYEMPAFTAELTA	
Qy 126LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKN 177	Db 607 ALYKNGSPVMYTYDEYQKGYLDQASGSAVIDLMENDQVWLQLPNSESNGLYSSEYV 662
KLLYNGRONYNPQTGIFTCEVPGVYYFAYHVHCKGG	Oy 228 -STFSGFI 234
QY 178 GQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKYSTFSGFII 235	Db 663 HSSFSGFL 670
	RESULT 7

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Gaps

509 125

83

625

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C; Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxylysin F;1-18/Domain: signal sequence #status predicted <SIG>F;1-18/Domain: anino-terminal (X) chain #status predicted <MAT>F;19-56/Domain: amino-terminal nonhelical #status predicted <NNC2>F;27-519/Region: interrupted helical #status predicted <NNC2>F;57-519/Region: interrupted helical #status predicted <NNC2>F;57-519/Region: interrupted helical #status predicted <NNC2>F;53-679/Domain: amino-terminal nonhelical #status predicted <NNC3>F;53-679/Domain: complement Ciq carboxyl-terminal homology <CIQ>F;517/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homolog C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homolog C;Keywords: collade coll; extracellular matrix; glycoprotein; homotrimer E;1-18/Domain: signal sequence #status predicted <SIG>F;19-674/Product: collagen alpha 1(X) chain #status predicted <MAT>F;547-673/Domain: complement Clq carboxyl-terminal homology <ClQ>
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R; Thomas, J.T.; Kwan, A.P.L.; Grant, M.E.; Boot-Handford, R.P.
Biochem J. 273, 141-148, 1991
A; Title: Isolation of cDNAs encoding the complete sequence of bovine type X collagen. A; Reference number: S13301; MUID:91113131; PMID:1703407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       510 PGPPGP-PGQAVMPEGFIKAGQRPSLSGTPLVSANQGVTGMPVSAFTVILSKAYPAIGTP 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKY--STFSGFIIYP 237
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C;Date: 21-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 PIGPPGIPGFPGSKGDPGS--PGPPGPAG-IATKGLNGPTGPPGPPGPPGPRGHSGEPGLPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              569 IPFDKILYNRQQHYDPRTGIFTCQIPGIYYFSYHVHVK---GTHVWVGLYKNGTPVMYTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 AQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKY--STFSGFIIYP
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36.8%; Pred. No. 5.9e-19;
tive 33; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78:
                                                                                                                                                                                                                                                                                                                                                                                                                                      27.7%; Score 362.5; DB 1; 36.8%; Pred. No. 3.9e-19; ative 33; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 1(X) chain precursor - bovine
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Best Local Similarity
Matches 86; Conserv
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A; Residues: 1-674 <THO>
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A; Residues: 561-647, (2,649-666 < AP2>
A; Residues: 561-647, (2,649-666 < AP2>
A; Residues: 561-647, (2,649-666 < AP2>
A; Residues: 561-647, (2,7); Rash, B.; Nicolai, H.; Jones, T.; Solomon, E.; Grant, M.; Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.; Solomon, E.; Grant, M.; Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.; Solomon, E.; Grant, M.; Title: The human collagen X gene. Complete primary translated sequence and chromosomal A; Reference number: 518249; MUID:92109659; PMID:1764025
A; Molecule type: DNA
A; Residues: 1-26, TY, 28-680 < THO>
A; Molecule type: DNA
A; Residues: 1-26, TY, 28-680 < THO>
A; Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 532-Ale R; Reichenberger, E.; Algner, T.; von der Mark, K.; Stoss, H.; Bertling, W.
Dev. Biol. 148, 562-572, 1991
A; Title: In situ hybridization studies on the expression of type X collagen in fetal hum A; Reference number: A43901; MUID:92077285; PMID:1743401
A; Molecule type: MRNA
A; Residues: 547-656 CRE2>
A; Note: sequence extracted from NCBI backbone (NCBIN:69012, NCBIP:69014)
B; Wallis, G.A.; Rash, B.; Sweetnan, W.A.; Thomas, J.T.; Super, M.; Evans, G.; Grant, M.; A.; Hum.; Genet. 54, 169-1718, 1994
A; Hum.; Genet. 54, 169-1718, 1994
A; Hum.; Genet. 54, 169-1718, 1994
A; Hum.; Genet. 54, 169-1718, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Cloning of human alpha-1(X) collagen DNA and localization of the COL10Al gene A;Reference number: S15826; MUID:91243838; PMID:2037056
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Cross-references: GB:S68531; NID:9545180; PIDN:AAC60615.1; PID:9545181
A;Note: mutant sequence from patient with metaphyseal chondrodysplasia type Schmid
A;Note: a second mutant sequence with 614-Pro is also described
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit ed and subsequently 0-91ycosylated.
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                                                                         N.Alternate names: procollagen alpha 1(X) chain
C.Species: Homo sapiens (man)
C.Species: The conversation of the conversation 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 'TIPFYGWYCLL',52-680 <APT>
A; Residues: 'TIPFYGWYCWVCLL',52-680 <APT>
A; Cross-references: EMBL:X65120; NID:923129
A; Cross-treferences: EMBL:X65120; NID:923129
A; Cross-the initial difference is probably due to translation of an intronic sequence R; Apte, S.; Mattei, M.G.; Olsen, B.R.
FEBS Lett. 282, 393-396, 1991
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A;Gene: GDB:COL10A1
A;Cross-references: GDB:128635; OMIN:120110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 6q21-6q22
A; Introns: 52/1
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10;

Gaps

42;

78

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A,Map position: 1p34.3-1p32.3
C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homolog
F;1-1L/Domain: amino-terminal nonhelical (fragment) #status predicted <NC2>
F;12-468/Region: interrupted helical
F;469-635/Domain: carboxyl-terminal nonhelical #status predicted <NC7>
F;508-634/Domain: complement Clq carboxyl-terminal homology <C1Q>
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                                                                                                                                                                                                 C;Accession: A57131
R;Muragaki, Y.; Jacenko, O.; Apte, S.; Mattei, M.G.; Ninomiya, Y.; Olsen, B.R.
J. Biol. Chem. 266, 7721-7727, 1991
A;Title: The alpha2(VIII) collagen gene. A novel member of the short chain col.
A;Reference number: A57131; MUID:91210292; PMID:2019595
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GLRRPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLM 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
A57131
collagen alpha 2(VIII) chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement subcomponent Clq chain C precursor - human N;Alternate names: complement subcomponent Clq gamma chain C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Accession: S14315; A03207 R;Sellar, G.C.: Blake, D.J.; Reid, K.B.M. Biochem. J. 274, 481-490, 1991
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                                                                                                                                                     RGGDGTSMWADLMKNGQVRASAIAQDADQNYD---YASNSVILHLDVGDEVFIKLDGGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M60832; NID:g177178; PIDN:AAA62822.1; PID:g177179
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A; Residues: 1-635 <MUR>
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109
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                                                                                                                                 C; Date: 22-May-1981 #sequence_revision 31-May-1996 #text_change 08-Dec-2000 C; Date: 22-May-1981 #sequence_revision 31-May-1996 #text_change 08-Dec-2000 C; Accession: B23422; A23422; B90304; A90301; B90315; A03206 R; Reid, K.B.M.

Biochem. J. 231, 729-735, 1985
A; Title: Molecular cloning and characterization of the complementary DNA and gene coding A; Accession: B23422
A; Molecule type: DNA
A; Residues: 'HS',1-32 < REI>A; Molecule type: DNA
A; Residues: 'HS',1-32 < REI>A; Molecule type: MRA
A; Residues: 'BS',1-32 < REI>A; Molecule type: MRA
A; Residues: 28-25 * REID: MOLECULE type: MRA
A; Residues: 28-25 * REID: MOLECULE type: MRA
A; Residues: 28-25 * REID: 
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Note: 176-C1x may also be present
C; Comment: The first component of complement is a calcium-dependent complex of the three ivation of C1x (enzyme), C1s (proenzyme), and the other eight components of complement.
C; Comment: The C1q subcomponent is composed of nine subunits, six of which are disulfide (see PIR:CIHUQC) chain. Equimolar amounts of the A, B, and C chains are found after reductions:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Map position: 1p36.3-1p34.1

C. Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal hom C. Superfamily: complement subcomponent Clq chain B; complement subcomponent C; superfamily: complement subcomponent Clq chain B #status experimental cMAT>
F; 1-27/Domain: signal sequence #status predicted <SIG.>
F; 28-253/Product: complement subcomponent Clq chain B #status experimental <MAT>
F; 33-116/Domain: collagenous, triple helix <COL>
F; 33-116/Domain: conplement Clq carboxyl-terminal homology <CLQ>
F; 249/Domain: complement Clq carboxyl-terminal homology <CLQ>
F; 249/Domain: conplement Clq carboxyl-terminal homology <CLQ>
F; 249/Domain: conplement Clq carboxyl-terminal homology <CLQ>
F; 259/Hodified site: pyrrolidone carboxylic caid (Gln) (in mature form) #status experiment F; 55, 65, 65, 83, 86, 101, 104, 107/Modified site: 5-hydroxylvsine (Lys) #status experimental F; 59, 62, 79, 98, 110/Modified site: 5-hydroxylvsine (Lys) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GEVGRRGKAGLRGPPGPPGPPGEPGRPGPPGPPGP-GPGGVAPAAGYVP
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A; Racidues: Protein
A; Residues: E', 29-84, D', 86-99, P', 101-135 <RE5>
R; Reid, K.B.M.; Thompson, E.O.P.
B; Reid, K.B.M.; Thompson, E.O.P.
A; Title: Amino acid sequence of the N-terminal 108 amino acid resis A; Title: Amino acid sequence of the N-terminal 108 amino acid resis A; Reference number: A90301; MUID: 79041552; PMID: 708376
A; Accession: A90301
A; Molecule type: protein
A; Reid, K.B.M.; Gaqnon, J.; Frampton, J.
Biochem. J. 203, 559-569, 1982
A; Title: Completion of the amino acid sequences of the A and B chance number: A90315; MUID: 82283890; PMID: 6981411
                                        - human
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                                complement subcomponent Clq chain B precursor [validated] N;Alternate names: complement subcomponent Clq beta chain
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Best Local Similarity 35.9%; Pred. No. 8.1e-19;
Matches 93; Conservative 34; Mismatches 90
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                                                                                                        ;Species: Homo sapiens (man);Date: 22-May-1981 #sequence_
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Similarity
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Best Local Simi.
Matches 84;
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A,Antone: 1036.3-1934.1
A,Antone: 1036.3-1934.1
A,Antone: 1036.3-1934.1
A,Antone: 1036.3-1934.1
C,Superfamily: Complement subcomponent Clq chain A; complement Clq carboxyl-terminal hom C; Reywords: complement pathway; glycoprotein; homodimer; hydroxylysine; hydroxyproline; C; Reywords: complement subcomponent Clq chain B #status predicted <NGP.
F; 12.9-45/Product: complement subcomponent Clq chain B #status predicted <WAT>
F; 29-245/Product: complement Clq carboxyl-terminal homology <ClQ>
F; 31-114/Domain: collagenous, triple helix <COL>
F; 31-134/Domain: complement Clq carboxyl-terminal homology <ClQ>
F; 32,Disulfide bonds: interchain #status experimental
F; 35,39,42.45,54.63,81,91,96,99,105/Modified site: 4-hydroxyproline (Pro) #status experimental
F; 57,72,75/Modified site: 5-hydroxylysine (Lys) #status experimental
                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-245 <SEL>
A; Residues: 1-245 <SEL>
B; Resid, K.B.M.
Biochem. J. 179, 367-371, 1979
Biochem. J. 179, 367-371, 1979
A; Title: Complete amino acid sequences of the three collagen-like regions present in sut A; Reference number: A90304; MUID:80020137; PMID:486087
A; Accession: A03207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein S; No. 10, N
                                              encoding the A-, B- and C-chains
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N.Alternate names: adipose specific collagen-like factor
C; Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Species: 10-May-1996 Seguence_revision 19-Jul-1996 #text_change 20-Sep-1999
C; Accession: JG4708; JG4944
R; Maeda, K.; Okubo, K.; Shimomura, I.; Funahashi, T.; Matsuzawa, Y.; Matsubara, K.
Biochen: Biophys. Res. Commun. 221, 286-289, 1996
A; Title: cDNA cloning and expression of a novel adipose specific collagen-like factor, A; Reference number: JC4708; MUID:96224171; PMID:8619847
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A;Residues: 1-244 <MAE>
A;Cross-references: DDBJ:D45371; NID:9871886; PIDN:BAA08227.1; PID:9871887
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A:Reference number: $14350; MUID:91174759; PMID:1706597 A; Sccession: $14351 A; Status: not compared with conceptual translation A; Status: DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 322; DB 1;
; Pred. No. 1.2e-16;
37; Mismatches 96;
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l Similarity 34.0%;
85; Conservative 3:
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VFSGFLLFPD 245
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Best Local S.
Matches 85
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A;Residues: 19-38;93-100;101-112;135-149;173-178 <NAK>
C;Comment: This protein is an endogenous factor that binds with a collagen-like domai
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL:X66295; NID:950228; PIDN:CAA46993.1; PID:950229
C; Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal
F;122-245/Domain: complement Clq carboxyl-terminal homology <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA clones coding for
A; Experimental source: adipose tissue R; Nakano, Y.; Tomita, M. R; Nakano, Y.; Tobe, T.; Chol-Miura, N. H.; Mazda, T.; Tomita, M. J. Biochem. 120, 803-812, 1996 A; Title: Isolation and characterization of GBP28, a novel gelatin-binding protein A; Reference number: JC4944; MUID:97103474; PMID:8947845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGAKGEVGRRGKAGLRGPPGPPGPPGEPGRPGPPGPPG-PGPGGVAPAAGYVPRIAF 112
                                                                                                                                                                                                                                                                                                                                                       C. Superfamily: unassigned collagens; complement C1q carboxyl-terminal homology C. Keywords: adipose tissue; glycoprotein; hydroxyproline C. Keywords: adipose tissue; glycoprotein; hydroxyproline F. 1-18/Domain: signal sequence #status predicted <SIG> F. 19-244/Product: gelatin binding 28kba protein #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVAPAAGYVPRIAFYAGLRRPHEGYEV----LRFDDVVTNVGNAYEAASGKFTCPMPGV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 YFFAYHVLMRGGDGTSMWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIK 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complement subcomponent C1q chain C - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C;Accession: 529328
R;Petry, F:; Reid, K.B.M.; Loos, M.
Eur. J. Biochem. 209, 129-134, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LLLLVAIPLLVHSSRGPAHYEMLGRCRMVCDPHGPRGPG-----PDGA----PASVPPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLLFLLALPLRSQASAG - - CYGIPGM - - - - - PGMPGAPGKDGHDGLQGPKGEPGIPAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;42-107/Region: collagen-like
F;142-107/Region: conplement Clq carboxyl-terminal homology <C1Q>
F;114-241/Domain: complement Clq carboxyl-terminal homology <C1Q>
F;95/Modified site: 4-hydroxyprolline (Pro) #status experimental
F;95/Modified site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82; Indels
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1larity 31.9%; Pred. No. 3.4e-16;
Conservative 38; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.3%; Score 318; DB 2; 34.3%; Pred. No. 2.4e-16; ive 36; Mismatches B2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 24.3%;
Best Local Similarity 34.3%;
Matches 92; Conservative 3
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Similarity
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Job time : 19 secs
   A; Residues: 1-245 <SEL>
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Matches
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A; Residues: 1-253 <SCH>
A; Cross-references: EMBL:X71127; NID:9510191; PIDN:CAA50440.1; PID:9510192
C; Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal hom
F; 121-249/Domain: complement C1q carboxyl-terminal homology <C1Q>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complement protein Clq beta chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 20-Aug-1999
C;Accession: 849158
R;Schwaeble, W.; Petry, F.; Loos, M.
submitted to the EMBL Data Library, March 1993
A;Description: cDNA cloning and expression of the mRNA encoding the B-chain of rat Clq.
A;Reference number: 849158
A;Reference number: 849158
A;Status: preliminary
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                                                                                                                                                                                                                                                                                   172 Y-----TSHTANLCVHLNINLARVASFCDHMFNSKQVSSGGALLKIQRGDEVWLSVN 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GEVGRRGKAGLRGPPGPPGPPGEPGRPGPPGPPGPGPGVGVAPAAGY--V 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIAFYAGLR-----RPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- RYKQKHQSVFTVTRQTTQYPEANALVRFNSVVTNPQGHYNPSTGKFTCEVPGLYYFVY
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91; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                  224 DYNGMYGIEGSNSVFSGFLLFPD 246
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                                                                                                                                                                                                                                                                                                                                                                                          216 GGKVHGGNTNKYSTFSGFIIYPD
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Matches 87; Conservative
                                                                                                      113 YAGLRRPH------
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subcomponent
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A;Residues: 131-171, N',173-177, W',179-239, 'ILPGFSA' <RE2>
C;Comment: The first component of complement is a calcium-dependent complex of the thivation of Clr (enzyme), Cls (proenzyme), and the other eight components of complement; c;Comment: The Clg subcomponent is composed of nine subunits, six of which are disulf (see PIR:CHHUQC) chain. Equimolar amounts of the A, B, and C chains are found after r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C. Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal C. Keywords: complement pathway; glycoprotein; heterodimer; hydroxylysine; hydroxyprol E;1-22/Domain: signal sequence #status predicted <SIGA = 23-245/product: complement subcomponent Clq chain A #status experimental <WAT> F;31-109/Domain: collagenous, triple helix #status predicted <CGL> F;24./Domain: complement Clq carboxyl-terminal homology <CIQ> F;26/Disulfide bonds: interchain (to chain B-31) #status experimental F;33-48,67,100,103/Modified site: 5-hydroxylysine (Lys) #status experimental F;33,48,67,100,103/Modified site: 4-hydroxyproline (pro) #status experimental F;39,45,54,57,73,85,97/Modified site: 4-hydroxyproline (Pro) #status experimental F;146/Binding site: carbohydrate (Asn) (covalent) #status experimental
R;Reid, K.B.M.
Biochem. J. 179, 367-371, 1979
A;Title: Complete amino acid sequences of the three collagen-like regions present in A;Title: Complete number: A90304; WUID:80020137; PMID:486087
A;Accession: A90304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLM-----KNGQVRASA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 CRMVCDPHGPRG----PGPDGAPASVPPFPPGAKGEVG-----RRGKAGLRGPPGPPG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 CRA---PDGKKGEAGRPGRRGR-----PGLKGEQGEPGAPGIRTGIQGLKGDQGEPG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 GFCDTTNKGLFQVVSGGMVLQLQQGDQVWVEKDPKKGHIYQGSEAD--SVFSGFLIFP 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 IAQDADQN--YDYASNSVILHLDVGDEVFIKLDGGKVH---GGNTNKYSTFSGFIIYP
                                                                                                                                                                                                                                                                                                                                                                                                                  B chains of
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                                                                                                                                                                                                                         A,Molecule type: protein
A;Residues: 23-96,'K',98-102,'P',104-130 <REI>
B;Reid, K.B.M.; Gagnon, J.; Frampton, J.
Biochem. J. 203;59-569, 1982
A;Title: Completion of the amino acid sequences of the A and A;Reference number: A90315; MUID:82283890; PMID:6981411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.0%; Score 314; DB 1; 36.6%; Pred. No. 4.7e-16; Live 23; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: GDB:ClQA
A;Cross-references: GDB:119042; OMIM:120550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2, 2003, 16:47:02
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A;Introns: 55/1
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TINS PAGE BLANN WEFTON

homo sapien mus musculu

homo sapien

mus musculu

xenopus lae cynops pyrr

OM protein

Run on:

sequence:

Searched:

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Minimum Maximum Database

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Q96a83 homo sapien
Q91vf6 mus musculu
Q77782 oryctolagus
Q9qxp7 mus musculu
Q76045 homo sapien
Q91718 xenopus lae
                                                         0920n0 tamias sibi
09h667 homo sapien
08te71 homo sapien
090412 brachydanio
                                                                                                                                                                                                                                                                                                                                           090w37 gallus gall
09nw37 gallus gall
09nw49 homo sapien
002802 homo sapien
061434 mus musculu
062001 mus musculu
                                                                                                                                                                                                                                                    062789 sus scrofa
08t018 drosophila
09tnf2 ascaris suu
09tum drosophila
063123 rattus norv
093419 gallus gall
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                                                                                                                     Q9bxx0 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 PHEGYEVLKFDDVVTNLGNNYDAASGKFTCNIPGTYFFTYHVLARGCDGTSMWADLCKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 PHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                 Q9w7r9
926n60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
44.5%; Score 584; DB 11; Length 120;
Best Local Similarity 89.2%; Pred. No. 1.7e-41;
Matches 107; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022724; AAH22724.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 AA; 13077 MW; CD72B2A353596525 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence
01-JUN-2002 (TrEMBLrel. 21, Last annotatin
Hypothetical 13.1 kba protein (Fragment).
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Q9W7R9
Q96A83
Q91VF6
O77782
Q9QXP7
O76045
                            Q99K41
Q9JHG0
Q920N0
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Q90412
Q9BXX0
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093419
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Q61434
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Q8T018
Q9NFZ9
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                                                                                                                                     133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                             NCBI_TaxID=10090;
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Q9D2V4;
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Q8R1Z2;
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Q9dZv4 mus musculu
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1581.910 Million cell updates/sec
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                                                                                                                                                                                          ......VHGGNTNKYSTFSGFIIYPD 238
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              GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Q9Z1K4
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_bacteria:*
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sp_rodent:*
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SEQUENCE
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KANAN CSTBL/63; TISSUB-KIDNEY;

KANAN JU, Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Radawa T., Hara A., Fukunishi Y., Konnó H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondó S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant H.,

Robin P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Robin P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Robin P., Boffelli D., Bojunga N., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Rownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Rostincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchlonni L., Mashima J., Marabaerts P.,

Rodon P., Ring B., Rinwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Ruzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Ruzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Ruzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Rusuki H., Radota K., Rawaji H., Kohtsuki S.,

Rusuki H., Radota K., Rawaji H., Kohtsuki S.,

Rusuki H., Radota K., Rawaji H., Radota K.,

Rusuki H., Radota K., Wang K.H., Weitz C., Willer K.,

Rusuki H., Radota K., Rawaji H., Kohtsuki S.,

Rusuki H., Radota K., Rawaji H., Kohtsuki S.,

Rusuki H., Radota K., Rawaji W., Kawaji H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 PGPPGPPG-PGPGGV----APAAGYVPRIAF------YAGLRRPHEG--YEV---- 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 DLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKY--STF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  620 AELTVPFPPVGAPVKFDKLLYNGRQNYNPQTGIFTCEVPGVYFAYHVHCKGG---NVWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 VCDPHGPRG----PGPDGAPASVPPFPPGAKGEVGRRGKAGLRGPPGPPGPPGEPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.3%; Score 397; DB 11; Length 744; 38.1%; Pred. No. 6.2e-25; Live 31; Mismatches 76; Indels 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01113; C1Q; 1.
SEQUENCE 744 AA; 73581 MW; C659BDCCBCD6EB9C CRC64;
(TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     744 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409:685-690(2001).

EMBL, AK018742; BAB31383.1; -.

MGD, MG188463; col8a1.

InterPro; IPR001073; clq.

InterPro; IPR000087; collagen.

Pfam; PF01391; Collagen.

Pfam; PF01391; Collagen; 7.

PRINTS; PR00007; COMPLEN
                                               Procollagen, type VIII, alpha 1
                (TrEMBLrel. 17 (TrEMBLrel. 17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity 38.18 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGFIIYP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGYLLYP 743
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                           NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             092158
0921588:___
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Best Local S
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Q921S8
ID Q921S
AC Q921S
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620 AELTVPFPPVGAPVKEDKLLYNGRQNYNPQTGIFTCEVPGVYYFAYHVHCKGG---NVWV 676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 DLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKY--STF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 VCDPHGPRG----PGPDGAPASVPPFPPGAKGEVGRRGKAGLRGPPGPPGPPGEPGR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46; Gaps
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.3%; Score 397; DB 11; Length 744; 38.1%; Pred, No. 6.2e-25; tive 31; Mismatches 76; Indels 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strougherg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013581; AAH13581.1; -.
InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF01386; C1q; 1.
Probom: PP000007; Collagen; 7.
Probom: PP000007; Collagen; 2.
PROSITE; PS01113; C1Q: UNKNOWN_1.
Collagen; Hypothetical protein.
                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (JUL.2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC011061, ABL1061.1;
InterPro; IPR001073; C19.
InterPro; IPR000087; C10.
InterPro; IPR000087; C10.
Pfam; PF00386; C19; 1.
Pfam; PF00391; C0llagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        744 AA; 73621 MW; BF7A7FD79D8463AA CRC64;
19, Created)
19, Last sequence update)
21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 73.4 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 30.3%; Score 397; DB Best Local Similarity 38.1%; Pred. No. 6.2e-Matches 94; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01113; C1Q; UNKNOWN_1.
                             01-DEC-2001 (TrEMBLrel. 19, Last 01-JUN-2002 (TrEMBLrel. 21, Last Procollagen, type VIII, alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGYLLYP 743
                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGFIIYP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo saplens (Human)
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE EROM N.A.
                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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80 PPGEPGRPGPPGPPG-PGP------GGVAPAAGYVPRIAFYAGLR-RPHEGYEV 125
                                                                                                                                                                                                STATEMENT STATEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 GPRG----PGPDG--APASVPPFP-----PGAKGEVG--RRGKAGLRGPPGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marks S.A., Lundmark C., Christersson C., Wurtz T., Odgren P.R., Selfert M.F., MacKay C.A., Mason-Savas A., Popoff S.E.; "Endochondral bone formation in toothless (osteopetrotic) rats: Int. J. Dev. Biol. 44:309-316(2000).

EMBL. AJ131848; CAA10518.1; -. InterPro; IPR001073; Clq.
InterPro; IPR001073; Clq.
InterPro; IPR001073; Clq.
Pfam; PF001386; Clq; 1.
Pfam; PF001386; Clq; 1.
Pfam; PF001986; Clq; 1.
SMART; SM00110; ClQ; L.
                                                                                                                                            RASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKY--STFSGFIIYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER 1 1
SEQUENCE 295 AA; 30012 MW; FF43B1548028813E CRC64;
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Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
MEDLINE-20310874; Pubmed-10853827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 35.**.
For B7; Conservative
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01-JUN-2002 (
01-JUN-2002 (
01-JUN-2002 (
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Q8TEJ5
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                                                                                                                                                                                                                                                                                                                          PG-PGPGGV-----APAAGYVPRIAF-YAGLRRPH------EGYEV------ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 GQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKY--STFSGFII 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 GPPGEPGRPGPPGPGPGVAPAAGYV-------PRIAFYAGLRRPHE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GYEV-LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Nielsen V.H., Bendixen C., Arnbjerg J., Sorensen C.M., Jensen H.E.,
A Nielsen V.H., Bendixen C., Arnbjerg J., Sorensen C.M., Jensen H.E.,
Shukri N.M., Thomsen B.;
Shukri N.M., Thomsen B.;
Tabnormal growth plate function in pigs carrying a dominant mutation
in type X collagen.";
In type X collagen.
In procons IPR001073; C10.
In therPro: IPR001073; C10.
In therPro: IPR001073; C10.
In pfam; PF01391; Collagen;
In procons; PR010007; Collagen;
In therPro: IPR00107; Collagen;
In therPro: IPR00107; Collagen;
In therPro: IPR00107; Collagen;
In therPro: IPR00107; C10.
In therPro: IPR00107; C1
                                                                                                                                                                                                                                                                           34 PHGPRG-PGPDGAPASVPPFPPGAKGEVGRRGKAGLRGPPGPPGPRGPPGRPGPPGPPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 GPRG----PGPDG--APASVPPFPPGAKGEVGR-------RGKAGLRGPPGPPR
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
Sus.
                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.7%; Score 363; DB 6; Length 679
36.4%; Pred. No. 3.9e-22;
tive 32; Mismatches 78; Indels
                                                                                    18.7%; Score 376; DB 4; Length 74.
11arity 37.2%; Pred. No. 3.5e-23;
Conservative 31; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       675 AA; 65447 MW; 26397B10310383F9 CRC64;
    73364 MW; 2BC1B0955DE2C9A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TN-2002 (TrEMBLrel. 21, Last annotation update)
Type X collagen.
COL10A1.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Best Local Similarity 36.4
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
744 AA;
                                                                                         Query Match
Best Local Similarity
Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 YP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collagen.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9N178
Q9N178;
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10;

Gaps

171

4

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57; Gaps

Indels

79;

No. 2.7e-20

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160 TVYMKD---VKVSLFKKDKAVLFTYDQYQERNVDQASGSVLLHLEVGDQVWLQVYEGENH 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Rachischmann W., Gassterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., A. Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchiondi L., Mashima J., Marchione P., Ring B., Ringwald M., Rodriguez I., Sakamcto N., A. Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wanshawashi H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wanshawashizaki Y.,
                                                                                                                                                             51 PFPPGAKGEVGRRGKAGLRGP-----PGPPGPRGPPGEPGRPGPPGPPGPGPGGVA 101
                                                                                                                                                                                                                                                102 PAAGYVPRIAFYAGLR-RPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHV 160
                                                                         3 LLLLVAIPLLVHSSRGPAHYEMLGRCRMVCDPHGPRG------PGPDGAPASVP
                                                                                                7 LILLLALP----SHGEDNWE------DPPLPKGACAGWMAGIPGHNGTPGR--
                                                                                                                                                                                                                                                                       LMRGGDGTSMWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVH
                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
35.4%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001).
EMBL; AK007683: BAB55187.1; -.
MGD; MGI:1916433; 1810033X05R1K.
InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Ffam; PF00138; C1q; 1.
Pfam; PF001391; Collagen; 2.
PRINTS; PR00007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 NGVYADNVND-STFTGFLLY 235
                                                                                                                                                                                                                                                                                                                                                                                                                              GG----NTNKYSTFSGFIIY 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-PANCREAS;
MEDLINE-21085660; Pubmed-11217851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
1810033K05R1k protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.1%;
                             92; Conservative
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         Best Local Similarity Matches 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                       161
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RA SACO C., Yasukawa Z., Honda N., Matsuda T., Kitajima K.;

RA Sato C., Yasukawa Z., Honda N., Matsuda T., Kitajima K.;

RA Sato C., Yasukawa Z., Honda N., Matsuda T., Kitajima K.;

RA "Identification and Adipocyte Differentiation-dependent Expression of Try The Unique Disialic Acid Residue in an Adipose Tissue-specific RT The Unique Disialic Adipo Q.";

RJ Biol. Chem. 276:28849-28856(2001).

BR FMEDI, AF269230, AAK58902.1;

DR FMEDI, AF269230; Caliq.

DR InterPro; IPR000087; Collagen.

DR Pfam; PF00386; Clq; 1.

DR Pfam; PF00391; Collagen; 1.

DR PFDDOM; PF01391; Collagen; 1.

DR PROSITE; PS01113; ClQ; UNKNOWN.1.

PROSITE; PS01113; ClQ; UNKNOWN.1.
                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGPRGPPGEPGRPGPPGPGPGPGVAPAAGYVPRIAFYAGLRRPHEGYE----- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 RGPAHYEMLGRCRMVCDPHGPRGP-GPDGAPA-SVPPFPPGAKGEVGRRGKAGLRGPPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----VLRFDDVVTNVGNAYEAASGKFTCPMPGVYFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         565 QFGLGELSAHATPAFTAVLTSPFPASGMPVKFDRTLYNGHSGYNPATGIFTCPVGGVYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AYHVLMRGGDGTSMWADLMKNGQVRASAIAQDADQNY-DYASNSVILHLDVGDEVFIKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DUN-2002 (TrEMBLrel. 21, Last sequence update)
Adipose tissue-specific protein adipo 0.
Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherlia; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
NOBI_TaxID-9913;
                                                                                                                                                                                                       Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.; "The nucleotide sequence of a long cDNA clone isolated from human
                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                              63;
                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 705;
                                                                                                                                                                                                                                                                                                                                                                         26.4%; Score 34.0.0,
35.6%; Pred. No. 1.2e-20;
+ive 30; Mismatches 77; Indels
                                                                                                                                                                                                                                                                    Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases EMBL; AK074129; BAB84955.1; -.
                                                                                                                                                                                                                                                                                                                                    705 AA; 67430 MW; 07DB85A65A948ED3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 GGKVHGGNTNKY--STFSGFIIYP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::| ::| |:||||:|| 681 SDQANGLYSTEYIHSSFSGFLLCP 704
    FLJ00201 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 35.69 nes 94; Conservative
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                  PISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                    spleen."
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Length 294;
30865 MW; 6D3905AE7C19E6FA CRC64;
                             DB 11;
                           Score 329;
                             Query Match
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6
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                                                                                                                                                                                                                                                                                                                                  112 FYAGLRRPHEGYEV------LRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYH 159
                                                                                                                                                                                                                                                                                                                                                                      95 PGPGGVAPAAGYVPRIAFYAGLRRPHEGYEV----LRFDDVVTNVGNAYEAASGKFTCP 149
                                                                                                           26
                                                                                                                                            42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 RGKQGPKGKAGAIGRAGPRGPKGVSGTPGKHGTPGKKGPKGKKGEPGLPGPCS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LLLLVAIPLLVHSSRGPAHYEMLGRCRMVCDPHG----PRGPG----PDGA----PASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 VLLLLALP------SHGQDTTTQGPGVLLPLPKGACTGWMAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 PPFP-----PGAKGEVGRRGKAGLRGPPGPPGPPGEPGRPGPPGPPG------
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-2122234; PubMed=11334417;
MEDLINE-2122234; PubMed=11334417;
Hotta K., Funahashi T., Bodkin N.L., Ortmeyer H.K., Arita Y.,
Hansen B.C., Matuzawa Y.;
Hansen B.C., Matuzawa Y.;
"Circulating concentrations of the adipocyte protein adiponectin a
decreased in parallel with reduced insulin sensitivity during the
progression to type 2 diabetes in rhesus monkeys.";
Diabetes 50:1126-1133(2001).
EMBL; AF404407; AAK92202.1;
InterPro: IPR001073; C1q.
InterPro: IPR001073; C1q.
Pfam; PF00386; C1q; I.
Pfam; PF01391; Collagen; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                  64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75; Indels
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodom; PD000007; Collagen; 1.
PROSITE; PS01113; C1Q; UNKNOWN_1.
SEQUENCE 243 AA; 26264 MW; 49A45DAF2B4613FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
1e-19;
                                                                                                  26 GRCRMVCDPHGPRG-PGPDGAPASV-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.1%; Score 316; DB 6; 33.1%; Pred. No. 9.7e-19;
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     32.7%; Preq. ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 VHGGNTNKY---STFSGFIIYPD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 QNGLEYDPYWTDSLETGELIYAD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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Best Local Similarity 33.18
Matches 90; Conservative
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae; Macaca.
NCBI_TaxID=9544;
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TISSUE-ADIPOSE TISSUE;
                 Similarity
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01-JUN-2002
              Best Local
Matches 8
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Arakawa T., Shinagawa A., Shinata K., Yoshino M., Itoh M., Ishii Y.,
Rawai J., Shinagawa A., Shinata K., Yoshino M., Itoh M., Ishii Y.,
Ra Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Aito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Ra Saito T., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ra Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ra Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L., M., Staubli F., Sizuki R., Tomita M., Ragner L., Washio T.,
Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ra Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Ra Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Ra Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Willming L.,
Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                      150 MPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 GWGLPGPSGPLGDSGPQGLKGVKGNPGNIRDQPRPAFSAIRQNPMTLGNVVIFDKVLIN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 GRPGPPGPPGP----GPGGVAPAAGY-----VPRIAFYAGLRRPHEGYEVLRFDDVVTN 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 VCDPHGPRGP-GPDGAPASV-PPFPPGAKGEVGRRGKA----GLRGPPGPPGPRGPPGEP
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection."; Nature 409:665-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 245;
                                                                                                                                                                                                                                                 01-JUN-2001 (TIEMBLIEL. 17, Created)
01-JUN-2001 (TIEMBLIEL. 17, Last sequence update)
01-JUN-2001 (TIEMBLIEL. 17, Last annotation update)
Complement component 1, q subcomponent, alpha polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01113; CiQ; 1.
SEQUENCE 245 AA; 25974 MW; 41C2066D49592020 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.0%; Score 302; DB 11; 37.3%; Pred. No. 1.5e-17; ive 27; Mismatches 79;
                                                                           210 VFIKLDG-GKVHG--GNTNKYSTFSGFIIYPD 238
                                                                                                 210 VWLQVYGEGERNGLYADNDNDSTFTGFLLYHD 241
                                                                                                                                                                                                                  245 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-KIDNEY;
MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:88223; Clqa.
InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
Pfam; PF00386; Clq; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK002655; BAB22262.1;
EMBL; BC002086; AAH02086.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 37.39
Matches 87; Conservative
                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki Y.;
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                                                                                                                                                                                                                09DCM6
                                                                                                                                                                          RESULT
Q9DCM6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 VPGVYYFAVHATVY---RASLQFDLVKNGQSIASF-----FQYFGGWPKPASLSGGA 195
                    VGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADL-----MKNGQVRASAIAQD 188
                                          140 QESPYQNHTGRFICAVPGFYYFNFQVI-----SKW-DLCLFIKSSSGGQPRDSLSFSN 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAIAQDADQNYDY-----ASNSV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 PGQPGLPGT--PGHHGSQGLPGRDGRDGRDGAPGEKGEGGRPGLPGPRGEBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGPDGAPASVPPFPPGAKGEVGRRGKAGLRGPPGPPGPRGPPGEPGRPGPPGPPGP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 GP-GGVAPA--AGYVPRIAFYA---GLRRPHEGYEVLRFDDVVTNVGNAYEAASGKFTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                              189 ADQN--YDYASNSVILHLDVGDEVFIKLD--GGKVHGGNTNKYSTFSGFIIYP 237
                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                         OBR002:
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to DKFZP586B0621 protein (Hypothetical 25.4 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 22.5%; Score 295; DB 11; Length 243; Similarity 36.4%; Pred. No. 5.5e-17; 36.4%; Oonservative 27; Mismatches 79; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Collagenous repeat-containing sequence of 26kDa protein.
CORS OR CORS26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC023068; AAH23068.1; -.
EMBL; BC025174; AAH25174.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 243 AA: 25420 MW; 498129CD051DB97B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 ILHLDVGDEVFIKLDGGKVHG--GNTNKYSTFSGFIIYPD 238
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MEDLINE-21264842; Pubmed-11071891;
Maeda T., Abe M., Kurisu K., Jikko A., Furukawa S.;
                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (FEB-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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Matches
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Q9ES30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 RGPPGEPGRPGPPGPPG-PGPGGVAPAAGYVP---RIAFYAGLRRPHEGYEV-LRFDDVV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 LGPRGERGQHGPKGEKGYPG------VPPELQIAFMASLATHFSNQNSGIIFSSVE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 INVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAIAQDADQN 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 CRMVCDPHGPRG----PGPDGAPASVPPFPPGAKGEVGRRGK-----AGLRGPPGPPGP 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 CSKCC--HGDYGFRGYQGPPG----PPGPPGIPGNHGNNGNNGATGHEGAKGEKGDKGD 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91
               encoding a putative secretory protein and its possible involvement in skeletal development."; J. Biol. Chem. 276:3628-3634(2001).

EMBL; AF246265; AAG33704.1; -.
MGD; MGI:1932136; Cors.
InterPro; IPR001073; Clq.
InterPro; IPR001073; Clq.
Pfam; PF01391; Collagen. 1.
PFNINTS; PR000107; CompLENNTC1Q.
SMART; SM00110; Clg; 1.
PROSITE; PS01113; Clq; 1.
SEQUENCE 246 AA; 26628 MW; 42A481B3E9F48F7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 PRGPGPDGAPASVPPFP----PGAKGEVGRRGKAGLRGPPGPPGPPGPPGPPGPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB-ADIPOSE TISSUE;

TISSUE-ADIPOSE TISSUE;

A Rabit M., Anantharayan S., Ionut V., Kim S.P., Van Citters G.W.,
A Rabit M., Bergman R.N.;
Dea M.K., Bergman R.N.;
T. "Regulation of Adiponectin gene expression in the fat-fed dog.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
L. Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
R. EMBL; AF417206; AAL007702.1;
R. InterPro; IPR001073; C19.
R. InterPro; IPR001073; C19.
R. Pfan; PF00386; C19; 1.
R. Pfan; PF00386; C19; Collagen; 1.
R. Pfan; PF00307; Collagen; 1.
R. PRODGM; PD000007; Collagen; 1.
R. PROSITE; PS01113; C10; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 21.5%; Score 282; DB 6; Length 194;
Best Local Similarity 36.8%; Pred. No. 5.2e-16;
Matches 70; Conservative 28; Mismatches 78; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Ćhordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
'Molecular cloning and characterization of a novel gene, CORS26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 2,46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 YDYASNSVILHLDVGDEVFIKLDGGKVHGGNTNKYSTFSGFIIY 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 SDTSSNHAVLKLAKGDEVWLRMGNGALHGDH-QRFSTFAGFLLF 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20890 MW; 3AA3D947D187AF9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83;
                                                                                                                                                                                                                                                                                                                                                                                                                                             22.3%; Score 292; DB 1 33.9%; Pred. No. 1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

22.3%; score 2.1. 1-16

Best Local Similarity 33.9%; Pred. No. 1e-16

Matches 76; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel. Adiponectin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
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SEQUENCE
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Q95J95
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PPG----PGPGGVAPAAGYVPRIAFYAGLRRPHEGYEV-LRFDDVVTNVGNAYEAASGKF 146
                                                      68 PRGFPGTPGRKGEPGESAYVHRSAFSVGLESRITVPNVPIRFTKIFYNLONHYDGTTGKF 127
                                                                                                                      55 GAKGEVGRRGKAGLRGPPGPPGPPGEPGRPGPPGPPGP-GPGGV--APAAGYVPRIA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 ADLMKNGQ----VRASAIAQDADQNYDYASN-----SVILHLDVGDEVFIKLDGG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 TCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 FYAGLRRPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTSMW 171
9 PKGACP-GWMAGIPGHPGHNGTPGRDGRDGTPGEKGEKGDPGLVGPKGDTGETGVTGVEG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                      Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
PROSITE; PS00445; FGGY_KINASES_2; UNKNOWN_1.
SEQUENCE 347 AA; 35928 MW; 1AFAB73C44E6F09C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 19.9%; Score 260.5; DB 4; Best Local Similarity 35.8%; Pred. No. 6.4e-14; Matches 72; Conservative 28; Mismatches 80;
                                                                                                                                                                                                                                                                                           347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: June 2, 2003, 16:46:39 Job time: 34 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 KVHGGNTNKYSTFSGFIIYPD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
InterPro; IPR000577; FGGY_kin.
                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                     GDEVFIKLDG 216 ·
                                                                                                                                                                                         ||:|:::: |
GDQVWLQVYG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                     207
                                                                                                                                                                                                                                                                                          941960
                                                                                                                                                                                                                                                      RESULT 15
Q96IH6
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